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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:		ixammer = :	Date:
Art Unit:	Phone Number 30	Examiner # :Serial Number:	
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If more than one searc	ch is submitted, please	prioritize searches in order of ne	ed.

Please provide a detailed stat	ement of the search topic, and	describe as specifically as possible the sub-	ect matter to be searched.
include the elected species of	r structures, keywords, synony	rms, acronyms, and registry numbers, and cospecial meaning. Give examples or relevan	ombine with the concept or
known Please attach a copy	of the cover sheet, pertinent cl	special meaning. Give examples or relevan	citations, authors, etc. if
Title of Invention:			
Inventors (please provide i	ull names):		
Inventors (please provide f	full names):		7,
Inventors (please provide f	ull names):		5
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Jan Delaval
Reference Librarian
Blotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

STAFF USE ONLA	Type of Search	Vendors and cost where applicable
Searchera_	NA Sequence (#)	SŤN
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Oy 943 GGACGAGGACGACCTACAGCTCAGCAGCACCTGAGGCTGAGGAAAGCAGACTA 1002 	003 CGAGAAACACAAAGTCTACGCGAAGTCACCCCATCAGGGCCTGAGCTCGCCGTCAC 1062	ACAGGGACCTACCCT 118 CAGGGGACCTACCCCT 217	Db 2179 ATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCTCCTCCTCCTTCGGTTTAATTAT 1242	OY 1243 GCTAATGTTGGAGGAGAATGAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTT 1302	OY 1303 TCCTCATTAATAATATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGA 1362 [QY 1363 CTAAATATGTAGTCGTCAAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATT 1422	Oy 1423 TTACCCTATCATCCTGCAAGACAGTCCTCCAAACCCACAAGCCTTCTGTCCTCAC 1482	Oy 1483 AGTCCCTGGGCCATGGTAGGAGAGACTTGCTTCCTTGTTTCCCCTCCTCAGCAAGCCC 1542	Qy 1543 TCATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCT 1602	QY 1603 GGGAATCAACAAAGGAAATTTTTCAAAAGAAAACTGCTATAAAAGAAAATAATTTTCAAAAGAAAACTGCTATAAAAGAAAAGAAATTTTCAAAAGAAAACCTGCTATAAAAGAAATTTTCAAAAGAAAACCTGCTATAAAAGAAATGATCATTCAT	Qy 1663 TGCAACATGATATAAAATAACAACAATAAAAGCAATTAAATAAA	Qy 1723 AIGTITAAGITCATGATACTIAGACTTAATGGAAIGTCAIGCCTIATTIACAITIT 1782 Db 2719 AIGTITAAGITCAIGGIACTTAGACTTAATGGAATGTCAIGCCTIAITTACAITIT 2778	Qy 1783 AAACAGGTACTCAGGGACTCCTGTCTGCCAAGGGCCGTATTGAGTACTTTCCACAACCTA 1842	Oy 1843 AITIAAFCCACACTATACTGTGAGAITAAAAACAITCATTAAAATGTTGCAAAGGTTCTA 1902	Qy 1903 TAAAGCTGAGACAAATATATTCTATAACTCACAATCCACTTCTAG 1951 	RESULT 2 AP001215 LOCUS AP001215 37201 bp DNA linear PRI 26-MAR-2002
FEATURES Location/Qualifiers source 1. 8858 Organism="unknown" 2396 a 2124 c 1950 g 2387 t 1 others ORIGIN	Query Match Best Local Similarity 90.6%; Pred. No. 0; Best Local Similarity 90.6%; Pred. No. 0; Matches 1783; Conservative 0; Mismatches 137; Indels 49; Gaps 4; 9 ACCATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTATGGGTATCTGGACCTGT 68	1002 ACCATGGAAGCCCCAGGTCAGGTTCTCTTCCTGCTACTCTGGCTCCCAGATACCACC 1061 69 GGGACATTGTGCTGACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGGGCC 128 1062 GGAACATTGTTCTAGTTCTCCAGATTCCTTGTTTTGTAAGCTTAGGAAAATTGTTCTAGTAGACAAAAAAAA	ACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAAACTACTTG	189 GCTTGGTACCAGCAAACCAGGCAGCCCCTAAACTGCTGATCTACTGCGCATCCACT 248 1164 CACTGGTATCAACAAAAATCACAGGGCACCTCCAAGGCTTCTCAATATATGCTTCCAT 1223		ATA 3 ACAGC 1	GTCTCT	ATGACG	463 TGGCCATTCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCC 522 	AGGGGG 582	AAGCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCTTGCTAT 6	AATTATCTGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCGG 7 AATTATCTGGAAAAAGCATGCTGTTTTTCTGTCTGTCCCTAACATGCCCTTATCTGTCTGTCCTGTC	CAAACAACACCCAAGGGCAAACTTTGTTACTTAAACACCATCCTGTTTGCTTTCTTT	CTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCCATCTGATGAGCAGTTGAA 82	ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAGGT ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGGT ATCTGGAACTGCTTGTTGTGTGCTGCTTGCTGAATAACTTCTATCCCAGAGGGCCAAAGGT	883 ACAGTGGAAGGTGGATAACGCCTCCCAATCGGGTAACTCCCCAGGAGAGTGTCACAGAGC 942

repeat_region complement(1283813137) /evidence=not_experimental /rpt_family="AluSq" repeat_region complement(1344513637) /evidence=not_experimental /rpt_family="I2" repeat_region 1363813914 /evidence=not_experimental /evidence=not_experimental	/rpt_family="Aluūb" repeat_region complement (1391514214) complement (1391514214) rpt_family="12" complement (1422014318) complement (1422014318) repeat_region rep	repeat_region complement(1437514543) evidence=not_experimental rpt family="LiM4" repeat_region complement(1454415508) repeat_region route family="L2" repeat_region 1584415918 repeat_region		repeat_region 19701030 /evidence=not experimental /rpt family="(TCCA)n" complement (1812618261) /rowidence=not experimental /rpt family="f2" repeat_region 1850018640		repeat_region Configuration (24*24*) repeat_region /rpt_family="MIR" repeat_region 2434. 25635 repeat_region 27443. 27466 repeat_region 27443. 27466 repeat_region 27886. 27918 repeat_region 27888. 27918	/evidence=not_experimental /rpt_family="\(\frac{7TTTTA}\)n" 28395. 28445 /evidence=not_experimental /rpt_family="\(\frac{7TTTTA}\)n" repeat_region 29384. 2947 Exich" repeat_region 1752. 31782 /rotdence=not_experimental /rpt_family="\(\frac{7T}\)rich" /rpt_family="\(\frac{7T}\)rich" /rpt_family="\(\frac{7T}\)rich" /rpt_family="\(\frac{7T}\)rich" /evidence=not_experimental /rpt_family="\(\frac{7T}\)rich" /evidence=not_experimental /rpt_family="\(\frac{7T}\)rich" /rpt_family="\(\frac{7T}\)rich" /rpt_family="\(\frac{7T}\)rich"
DEFINITION Homo sapiens genomic DNA, chromosome 2p11.2, clone:cos141. ACCESSION AP001215 KEYWORDS KEYWORDS SOURCE Homo sapiens DNA, clone:cos141. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE 1 AUTHORS Shimizu, N. and Kawasaki, K. AUTHORS Shimizu, N. and Kawasaki, K. AUTHUB Homo sapiens genomic DNA, chromosome 2p11.2, clone:cos141 JOURNAL Published Only in Database (2000) REFERRNCE 2 (bases 1 to 37201) AUTHORS Shimizu, N. and Kawasaki, K. AUTHORS Shimizu, N. and Kawasaki, K. AUTHUB Direct Submission JOURNAL Submitted (21-FEB-2000) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Balology; 35 Shimanomachi, Shinjuku-ku, Tokyo	Tel: 81-33-351-2370, Fax: 81-3-3351-2370) COMMENT On Sep 13, 2000 this sequence version replaced gi:8096503. FEATURES Location/Qualifiers Source 0.237201 0.23	/clone="cos141" repeat_region 184492 /rpt_family="Aluy" repeat_region 12771297 /rot_family="Aluy" /rot_family="Aluy" /rot_family="Aluy"	region	repeat_region acse. : 8394 repeat_region repeat_region		repeat_region 10763 .10936 . voidence=not experimental / rot dence=not experimental / rot dence=not experimental / rot family="GA-rich" 1143 .11600 . voidence=not experimental / rot family="MIR" ropeat_region 11733 .12023 . repeat_region / rot family="MER3" / rot family="MER3" / rot family="MER3" / rot family="MIR" / rot famil

Db 6101 GGAGAAGTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Oy 1453 CCCTCAAACCACACACCTCTGTCCTCACAGTCCCCTGGGCCATGGTAGACACTCT 1512	6641 A 6641 A 1693 A 6701 A 6761 A 6761 A 1813 A 6621 A		LOCUS LOCUS AC104601 DEFINITION Nome sapiens chromosome 2 clone RP11-1435C3, WORKING DRAFT ACCESTON AC104601. VERSION KEYWORDS HOMO sapiens CONGANISM REFERENCE AUTHORS WALCTSCON NA LO 166276)
repeat_region /revidence=not_experimental /refeat_region /35753366	, Gaps GAGTTT 49 GAGTTT 55 GAGTTT 55	5561 613 5621 673 5681 733	CTGCT 8 CTGCT 5 CTGCT 5 CAATC 9 CTCAG 9	-

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                                                                                        Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 166276;
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 166276)
Waterston, R.H.
Direct Submission
Submitted (13-DEC-2001) Genome Sequencing Center, Washing
University School of Medicine, 4444 Forest Park Parkway, M
                                                                                                                                                              Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                          Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 165062 bases at least Q30
Consensus quality: 165366 bases at least Q30
Consensus quality: 165364 bases at least Q30
Insert size: 166000; agarose-fp
Insert size: 166000; sum-of-contigs
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                                                                                                                                                                                                Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                    Genome Center ------
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/note="assembly_name:Contig11"

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Best Local Similarity 99.9%; Pred. No. 0;
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                                                                    145584 GIGAATCTTTGCACCTGTGGTTTCTCTCTTTCTCTTTTAATAATTATTATCTGTTGTTTT
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                                                                                                                                                                144924 TITAAATACGCTTCTTGGTCTCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTTCTG
                                                                                                                                                                                                                                                                                                                                                              144984 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCCAAGGGCAGAACTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      145044 TACTTAAACACCCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCTGGGCCATGGTAGGAGAGACTTG
                                                                                                                                        CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAGAAACTCAAAACTTCAAGAT
                                                                                                                                                                                                                                  TITIAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG
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                                                                                                                                                                                                                         AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 1932
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AC096579 AC022416
HTG06579.1 GI:15628889
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Materston,R.

Direct Submission

Direct Submission

Submitted (01-MAR-2002) Department of Genetics, Washington
Submitty, 4444 Porest Park Avenue, St. Louis, Missouri 63108, USA

On Sep 18, 2001 this sequence version replaced g1:7705152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 176555)
The sequence of Homo sapiens BAC clone RP11-601N4
The sequence of Homo sapiens BAC clone RP11-601N4
Thubblished (2001)
3 (bases 1 to 176555)
Waterston, R. H.
Submitted (18-SBP-2001) Genome Sequencing Center, Washington Nulversity School of Medicine, 4444 Forest Park Parkway, St. Louis, Ac. (bases 1 to 176555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGGCT
                               AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.

Homo sapiens
Eukaryota; Matazoa; Chordata; Craniata;
Mammalia; Eutheria; Primates; Catarrinii
I (bases I to 176555)
Sulston,J.E. and Materston,R.
Toward a complete human genome sequence
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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                 this
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION;
The clone sequenced to the left is RP11-450E9; the clone sequenced to the right is RP11-685N3. Actual start of this clone is at base position 1 of RP11-601N4; actual end is at base position 176555 of RP11-601N4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date from AC062029 and AC060807 was used to finish this clone, AC023416. Polymorphisms have been identified between AC023416 and AC062029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     f one male
Frengen, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RPC1-1 human BAC library was made from the blood of one adonor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Freng Tateno.M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de ABCCTOR: pBACC3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of AC023416 has been incorporated into AC096579.
Location/Qualifiers
1. 176528
/ organism="famo sapiens"
/ db xref="taxon:9606"
/ chromosome="2"
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/dlone="rep1"-61N4"
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/note="match to EST
3289. 3365
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207. .1364
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1425. .1774
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942. .2293
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2393. :2488
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/note="match t
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source 1.2737 /organism="Homo sapiens" /b xref="teaxon:9606" /cell_line="Cors." /cell_tine="Cors."	/tissue type= chimeria: /tissue type="nasopharyngeal carcinoma" <339>656 /note="expressed in nasopharyngeal carci	/product="imminoglobulin kappa chain constant region" /protein id="AAB17008.1" /protein id="Isla996" /protein id="Isla996" /translation="Isla996"	ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC RGEC" BASE COUNT 820 a 645 c 536 g 736 t	Oxigin Query Match 77.3%; Score 1514.2; DB 9; Length 273 Best Local Similarity 99.8%; Pred. NO. 0; Marches 1516; Conservative 0; Mismarches 3; Indels 0	CTCTGAGGGGGTCGGATGACGTGCCATCTTTGCT	4 6 4	553	613	673		793	QY 853 GAATAACTICTATCCCAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC	Oy 913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGGAC	OY 973 CAGCACCCTGACGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 	Qy 1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG Db 602 CACCCATCAGGGCCTGAGCTCGACCTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG	QY 1093 GGAGAAGTGCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCTCCCATCCTTTGGCCTC	Qy 1153 TGACCTTTTTCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCTCTCT
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Director Submitted (13-007-2000) Molecular Biology Laboratory, Cancer Research Institute of Hunan Medical University, 88 Xiangya Road, Changsha, Hunan 410078, People's Republic of China Sequence update by submitter

E 7 (bases 1 to 7810)

S wei,L., Ming,L., Wei,L. and Ya,C.
Direct Submission

L Submitted (10-ARR-2002) Molecular Biology, Cancer Research Institute, Xiangya Medical School of Central South University, 88 Xiangya Road, Changsha, Hunan 410078, People's Republic of China Sequence update by submitter

Sequence update by submitter

On Jun 26, 2002 this sequence version replaced gi:10800410.
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kb fragment sequence of Nasopharyngeal
                                                              Wei,R., Ming,L., Linqing,X., Xinxian,W., Wei,L. and Ya,C.
Nuclectide sequence analysis of Tx, a transforming gene isolated
From a masopharyngeal carcinoma cell line CNE2
Unpublished
(bases 1 to 7810)
                                                                                                                                                                                                                                                                Submitted (19-AUG-1999) Molecular Biology Laboratory, Cancer Research Institute of Hunan Medical University, 88 Xiangya Road, Changsha, Hunan 410078, People's Republic of China (bases 1 to 7810)
Wei,L., Ming,L., Wei,R., Xinxian,W., Lingqin,X. and Ya,C.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 7810)

Ming, L., Wei, R., Xinxian, W., Linqing, X., Wei, L. and Ya, C.

Nucleotide sequence analysis of a transforming gene isolated from asopharyngaal carcinoma cell line CNB2: an aberrant human immunoglobulin kappa light chain which lacks variable region

DNA Seq. 15, 1-5 (2002)

2 (bases 1 to 7810)

Ming, L., Wei, R., Wei, L., Xinxian, W., Lingqin, X. and Ya, C.
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/rpt family="LiMA2" on complement(36643. 36737) /rpt family="WRR" on complement (37348. 37462)							/rpt_ramily="MEK5B" on_complement(41471, .41683)								/rpt_family="L1ME3A" on complement(4735847473)			on complement(4778847950) /rot familv="L1MD1"		on Complement (48303)	48600 .48980						/note="similar to EST with GenBank Accession Number		29895	/rDc_remily="Alu-1" on 65515, 62899 /note="finite to RST with GenBank Accession Number	AA295982"				. • `	/ ipc _ rauniy= _ nimpi. on 6563965692
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/rpt_family="MER82" complement(86679323) /rpt_family="TIGGER1" complement(93589399)	ot_family="LIPA7" nplement(9400, 11092)	OC.IMMILY="ILGGERI" 13511550 TF family="MEDRO"	506. 11191 108. family="n."	nplement(11935, 12360)	28412473 12473	nplement(1263) . 12760)	J. L.	July 134613 Flame 1 (13462) 13509)	Jan. 115. 115. 115. 116. 116. 116. 116. 116	or_ramily="b1" pplement(14511, .14815)	U	t tamily="L1" 049. i5924	ot tamily="LIMB7" npTement(1725417323)	ot_tamily="LiME3A" 86418064	ot family="L1" 166. 18751	ot_family="L1PA15" 44218941	family="LiPA11"	nplement(1918819537) bt_family="MLT1A"	13519900 br familv="11MC4"	742 . 23919 142 2319	007. 24914 t family	71. 25.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00		c_ramily="Li" 17926599	ot family="L1" 11326666	t family="1.1" noTement(26822, .27169)	t_family="HERVL" 77228105	ot family="MER444A" plement(2881628910)	of family="Alu-S"	/rpt family="Alu-Sz" complement(2961529915)	ot_family="L1" 118, 30539	/rpt_family="LIPA7" complement(29980. 30316)	/note="similar to EST with GenBank Accession Number F06637"	3093631317 /rot family="L1"	3135032223 /rpt familv="1.1"	3222433318
/rpreser_region com repeat_region com		/rp repeat_region 111	repeat_region 116	repeat_region com	repeat_region 123	repeat_region com	repeat_region com	repeat_region com	repeat_region com	repeat_region com	repeat_region 148	/rp repeat_region 150	/rp repeat_region com	/rp repeat_region 178		/rp repeat region 188			repeat_region 196	repeat_region 238	repeat_region 245	repeat_region 251	repeat_region 255	/rp repeat_region 264										repeat_region 309	repeat_region 313	repeat_region 322

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Unclassified.
Unclassified.

1 (bases 1 to 1701)

Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
Antl-CD4 antibody homologs useful in prophylaxis and treatment of
AIDS, ARC and HIV infection
Patent: US 5871732-A 54 16-FEB-1999;
Location/Qualifiers

1. 1701

/organism="unknown"

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                                63206 CTICCTIGITITICCCCTCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT
                                                                                                 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT
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191 TTGGTACCAGCAGAAACCAGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAG 250	280 GGAATCTGGGGTCCCTGATCGTTTCTCAGGGGGGGGGGG		431 GAMATICTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT 490	491 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAAGAGCTCCAACAA 550 	551 AACAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAAGAACTCAAAACATCAAG 610 	611 ATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC 670	671 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCCAAGGGCAGAACTTT 730 	731 GITACTTAAACACCAICCIGITTGCTICTTCCTCAGGAACIGIGGCIGCACCAICTGIC 790 	791 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 850 	851 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAAGGCCCTCCAA 910 	911 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCACGAGCACCTACAGCCTC 970	971 AGCAGCACCCTGACGCTGAGCAAAGCAGACACAAAGTCTACGCCTGCGAA 1030 	1031 GTCACCCATCAGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTAG 1090 1045 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTAG 1104	1091 AGGAGAAGTGCCCCACTGCTCCTCAGTTCCAGCCTGACCCCTCCCATCCTTTGGCC 1150	1151 TCTGACCCTTTTTCCACAGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTCACC 1210	,1211 TCACCCCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAAT	
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. HOZO H	HSIGKA ON H.sapi NX67858 X67858 IG kap Homo s	HSIGKA 5364 bp DNA linear PRI 16-OCT-1992 H.sapiens DNA for IG kappa JC region. X67858 K67858 IG:33217 IG kappa light chain. Homo sapiens.
REFERENCE AUTHORS	Eukary Mammal 3 1 (ba 5 Garrar	<pre>Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 5364) Garrard,W.T.</pre>
TITLE JOURNAL	Direct Submit Centre	Submission ted (23-JUL-1992) W.T. Garrard, UT Southwestern Medical Journal of Biochemistry, 5323 Harry Hines Blvd., Dallas as man
REFERENCE AUTHORS		Jess I to 5364) uurst.C., Henney, H.R., Max, E.E., Schroeder, H.W. Jr., 'F., Siminovitch, R.A. and Garrard, W.T.
TITLE	Nucleo immuno	tide sequence of the intron of the germline human kappa galobulin gene connecting the J and C regions reveals a matrix ation region (MAR) next to the enhancer
JOURNAL MEDLINE PUBMED	5 Nuclei 2 930272 0 140880	c Acids Res. 20 (18), 4929-4930 (1992) 1.17 1.8
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)	/organism="Homo sapiens" /db xref="taxon:9666"
misc	_feature	/germline 252 290 /notemili region"
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misc	feature	917. 955 /note="J3 region"
misc	fea	1252. 1290 note="J4 region"
misc		15701608 /note="J5 region"
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29-SEP-1999
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Burkly, L.C., Chisholm, P.L., Thomas, D.W., Rosa, M.D. and Rosa, J.J.
Anti-CD4 antibody homologs useful in prophylaxis and treatment of
AIDS, ARC and HIV infection
Patent: US 5871732-A 53 16-FEB-1999;
Location/Qualifiers
    204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC
                                                    TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTT
                                                               GCTTCCTTGTTTTCCCCTCCTCAGCAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT
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Pred. No. 6.4e-270;
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S ATAACTTCTATCCCAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 4 ATAACTTCTATCCCAGAGGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCCATCGG 5 GTAACTTCCAGGAGAGGTCACAGAGGACAGCACAGAACGGCCTCCAATCGG 6 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACATACAGCATCGCAATCGCAATCGCAGAACTCCCAGGAGAGTGTCACAGAGAGAG	0.95 CCATCAGGGCCTGAGCTCGCCGTCAAAGAGCTTCAAAGAGGTGTTAAAGGG	Db 744 ACCTITITICAL	1334 ACCAACTACTCAATTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC	Oy 1454 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCTGGGCCATGGTAGGACAGACTTGC 1513 Db 1043 CCTCAAACCCACAAGCCTTCTGTCTCTCACAGTCCCTTGGGTAGGACAGAGACTTGC 1102 Oy 1514 TTCCTTGTTTTCCCCTCCTCAAGCACCCCTTTTTAAGGGTCACAGGTCTTA 1573 Db 1103 TTCCTTGTTTTCCCCTCCTCACACAGCCTCTTTTTAAGGGTCAGACAGGTCTTA 1162 Oy 1574 CAGTCATATTTCAATTCCCTCCTCGGGAATCAACGCAAAATTTTCAAAAG 1633		HESTON: 12 HESTON: 12 HESTON: 12 HESTON: 1209 bp DNA linear PRI 07-JAN-1995 DEFINITION C-terminal part of human kappa-immunoglobulin gene coding for amino acids 109 to 214. ACCESSION VOOS57, 100241 VERSION CHOOS FOR LINE; IG Rappa light chain; immunoglobulin. KEYWORDS HOWN SAPIENS. HIGHER HIGHER HOWN. HIGHER HIGHER HOWN. TITLE TITLE TITLE TITLE TITLE TITLE TITLE TANNING HOWN SAPIENS. HIGHER HIGHER HOWN SAPIENS. HIGHER HIGHER HOWN SAPIENS. TITLE TITLE TITLE THE TITLE HOWN SAPIENS. HOWN SAPIENS. HIGHER HIGHER HOWN SAPIENS. HIGHER HIGHER HOWN SAPIENS. HIGHER HIGHER HIGHER HOWN SAPIENS. HIGHER

key from to description POLYA 813 813 poly adenylation site CDS 136 653 reading frame. Location/Qualifiers source /organism="Homo sapiens" /db xref="taxon:9606" /map="zpl="/tasue_type="placenta"	/germline join(K0135.1:1199,1656) /gin="IRKC" intron <1333 KC"	/gene="lokC" /note="kappa intron J-C" <334 . 656 /gene="lokC"	/ noce="C_region" / codon_start=3 / producf="immunoglobulin kappa chain" / protein_id="AAA58989.1" / db_xref="GI:185945" / dd_xref="GD:GO0-120-088" / translation="YPAAE9VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDN / translation="YPAAE9VFIPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDN ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	234 g 1t 700 bp a	Query Match 60.3%; Score 1181.2; DB 9; Length 1209; Best Local Similarity 99.6%; Pred. No. 7.1e-270; Matches 1205; Conservative 0; Mismatches 3; Indels 2; Gaps 2;	Oy 435 TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494	Qy 495 TGCAAGGTCAGAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGACTCCAACAAAACA 554	Qy 555 ATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAAGAACTCAAAACATCTA 614	Qy 615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 674	Oy 675 TGTCCCTAACATGCCCTGTGATTATCCGCAACACACCCCAAGGGCAGAACTTTGTTA 734	Oy 735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCACCATCTGTCTTCA 794	Qy 795 TCTTCCCGCCATCTGAAGAGAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854	OY 855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914	Oy 915 GTAACTCCCAGGAGAGTGTCACAGGACAGGAAGGACAGCACCTCAGCA 974	QY 975 GCACCTGAGCGAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034 DD 541 GCACCCTGACGCTGAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 600	
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495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554 	555 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 614	TAAATACGCTTCTTTGGTCTCCTTGCTATAATTATCTGGGGTAAAGCATGCTGTTTTCTGTC	TGTCCCTAACATGCCTGGTTTATCCGCAAACAACAACGCCAGGCCGTTTTTGTCCCCAGGCCCTAGGCGCTGTGTTATCTGCCCAGGCAGAACTTTGTTTATCTGCCAGGCAGAACTTTGTTTATATCTGCAGAACAACAACAACAACAACAACAAACA	CTTAAACATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGGCTGCACCATGTTTGTT	8 5 4	ATAACTICTATCCCAGAGGGCAAAGTACAGGGGAGGGGGTAACGCCTCCATCGG 91	GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGGACAG	504 GIAACICCCAGGGGGGGGCACAGGACAGGACAGGACAGG	GCATCATGAGGCAGAGGCACACACACACACACACACACAC	AGAAGTGCCCCCACCTGCTCCAGCTTCCAGCCTGACCCCTCCCATCGTTTGGCCTCTG	1155 ACCCTTTTTCACAGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1214	1215 CCCCTCCTCCTCCTTGGCTTTAATGTTGCTAATGTTGGAGGAGAATGAAT	1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTTTT 1333	1334 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGGGCATAAC 1393 	1394 CATITATAAAATCATCCTTCATTCTATTTTACCCTATCATCTCTGCAAGACGTCCTC 1453 	1454 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGACTTGC 1513	1514 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGTGACAGGTCTTA 1573
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Hilger, C., Grigioni, F. and Hentges, F.
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1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTCAAAAGA
                 1163 CGGTCATATATCCTTTGATTCCATGGGAATCAACCAAGGCAAATTTTTCAAAGA
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Hilger,C.
Direct Submission
Submitted (21-MAR-1996) C. Hilger, Centre Hospitalier, 4 Rue
Barble, L-1210 Luxembourg, LUXEMBOURG
Related sequences V00557 and J00241.
Location/Qualifiers
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Pred. No. 7e-244;
0; Mismatches 2; Indels 0;
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/product="kappa light chain constant region"
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/cell_type="peripheral blood lymphocytes"
/dev_stage="adult"
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1223 AGAAACCTGC 1232
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 672)

SK im, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and.

Kim, Y.S.

In Frontier Korean EST Project 2001

AL Unpublished (2002)

AL Unpublished (2002)

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Factoric Kim YS

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Fax: +82-42-860-4470

Fax: +82-42-860-4470

Fax: Had-anily sequence stop: 672.

High quality sequence stop: 672.
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F.EST0068215 S19N665307 Homo sapiens cDNA clone S19N665307-2-D11
S', mRNA sequence.
BM788938
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BQ008802 U
BM894026 i
BM991141 U
BM511847 i
BM510477 i
BQ008754 U
BQ573999 U
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BM819800 K-EST0087
BM510472 ij46b02.x
BM768769 K-EST0051
BQ049562 AGENCOURT
                                                                                         July 18, 2003, 04:16:54; Search time 3396.49 Seconds
(without alignments)
9345.860 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Score

Result No. 672 553.8 523.4 521.8 521.8

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..., catarthin; Hominidae; Buteleostom.

..., catarthin; Hominidae; Homo.

(b, K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Prontier Yocren EST Project 2001

**MINAL Unpublished (2002)

**ENT Contact Kim You Besident Strain Strain
                                                                                                                                                                                                                  BM819800 656 bp mRNA linear EST 06-MAR-2002 K-EST0087997 S16N667673 Homo sapiens cDNA clone S16N667673-2-G02 5', mRNA sequence.
BM819800.1 GI:19176213
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota, metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases I to 656)
1 (Dases I to 656)
0, K.J., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H. Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J. M., Park, H.S., Kim, S. and
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          1281
      1270 AAAGTGAATCTT
                                                       661 AAAGTGAATCTT
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                                                                                                                                          / Jab host="ToploF'"
/ Jab host="ToploF'"
/ Inote="Organ: Stemach; Vector: pCNS; Site 1: ECORI;
Site 2: NoII; The poly (A) + RNA was dephosphorylated with
batte_2: NoII; The poly (A) + RNA was dephosphorylated with
batte_1 alkaline phosphatase (EAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA liker including ECOR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coll NAI ligase after digestion of
ECORI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Toplof' by electroporation method.
The cDNA libraries constructed by this method are
full-langth enriched cDNA library. "
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Similarity 100.0%; Pred. No. 1.1e-127; Indels (2); Conservative 0; Mismatches O; Indels (
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/db xref="taxon:9606"
/clone="S19N665307-2-D11"
/clone_lib="S19N665307"
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Endocrine Pancreas Consortium
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Endocrine Pancreas Consortium
Barvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 552)
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Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript Sk- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40Up from Gibco
High quality sequence stop: 448.
5
220 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT
                                                                  GAATAACTICTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC
                                                                                                                                                                                                                                                                                                                                                                GAATAACTTCTATCCCCAGAGAGGCCAAAGTACAGGGAAGGTGGATAACGCCCTCCAATC
                                                                                                                         TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACCCCAAGGGCAGAACTTTGT
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HWAGE:5633978"
/clone=lib="Human insulinoma"
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Fax: 617-495-8557
Email: dmelton@bio
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(http://genome.wustl.edu/est/lambda_protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Buclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

1 118 C 162 g 154 t
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1 (bases 1 to 557)
Kim,'N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               950 AAGGACAGCACCTACAGCCTCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAA 1009
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/tissue_type="insulinoma"
//lab_host="DH10B (phage-resistant)"
//note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
Xho1; Site_2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 610)
S NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Low Stauth
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
http://image.llnl.gov
Clone distribution: MGC clone distribution information can be
http://image.llnl.gov
Plate: LLANLS977 row: p column: 13
High quality sequence stop: 595.
1. 610
Corganism="Homo sapiens"
Accation/Qualifiers
1. 610
Corganism="Homo sapiens"
Als boste="MpMCG" 85"
Clone="HAACO: 5606"
Clone="HAACO: 5606"
Clone="HAACO: 578516"
Average insert size 1.867 kb. Library enriched for full length clones and constructed by Life Technologies.
NOTE: Clone this is a NIH MGC Library."
NOTE: Clone this is a NIH MGC Library."
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126 THIIHHHIIHHHIHHHIHHHIHHHIHHHIHH
127 TGAACTGCTTCTTGTTGTGTGCCTGAATAACTTCTATCCCAAAGAGGCCAAAGTACA
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Unpublished (2002)

COURAL Unpublished (2002)

COURAL Unpublished (2002)

CORNAL Unstitute of Bioscience & Biotechnology

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

Tel: +82-42-860-4470

Tel: +82-42-860-4470

Email: yongsung@mail.kribb.re.kr

Plate: 11 zow: A column: 06

High quality sequence stop: 557.

Location/Qualifiers

1.0.557

Location/Qualifiers

(do.granism="stomo appiens"

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31 ACGAACTGTGGCTGCACCATTGTCTTCATCTTCCCGCCATCTGAGAGTTGAAATC 92
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1183 ATTGCGGTCCTCCAGCTCATCTTTCACCTCCCCCCCCTCCTTCGCTTTAATTAT 1242
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UI-CF-EC1-acd-g-18-0-UI.51 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-acd-g-18-0-UI 3', mRNA sequence.
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Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                        189 ACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGGA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 648)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                              309 CGAGAAAACACAAAAGTCTACGCATGCAAGTCACCCATCAGGGCCTGAGGTCGCCCGTCAC
                                                                                                                 GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGCATA
                                                                                                                                                          249 GGACAGCAAGGACACCACCTACAGCCTCAGCAGCCTGACGCTGAGCAAAGCAGACTA
                                                                                                                                                                                                     CGAGAAACACAAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAC
                                                                                                                                                                                                                                                                                              1063 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTC
                                                                                                                                                                                                                                                                                                                   CAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCT
                                                                                                                                                                                                                                                                                                                                                                                                           429 CAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGACCTACCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1243 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGNCCCT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
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/db xref="taxon:9606"
/dlone_inhed=102013"
/dlone_inhe="IMAGE 113"
/dlone_inhe="MIH MGC 113"
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ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5 adaptor:
GGGACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RI (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.

2. 1 (Dases 1 to 643)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Matson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arayed by: The I.M.A.G.B. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at:

thup://image.llnl.gov. d column: 01

High quality sequence stop: 594.
         1125
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         GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCCACCTGCTCCTCAGTTCCAG
                                                                                                               426 CCTGACCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT
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Best Local Similarity 99.4%;
Matches 523; Conservative
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 540)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly a trail. Tissue Procurement: Louis M. Standt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
COND Library Arrayed by: M.B. Soares Lab
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modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI_CFEEL is a normalized cDNA library containing the
following tissue(8): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome.Research, 6:791-806, 1996. First strand cDNA
Synthesis was primed with an oligo-dr primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, dispessed with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)B tail. The sequence tag for this library is
AAGTCCTTAC.
TAG ILB-UI-CF-ECI
TAG ILSUE-Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
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Location/Qualifiers

1. 540

1. 540

1. 540

2. coganism="Homo sapiens"

(db_xref="taxon:9606"

(dlone="IMAGE:3060557"

(clone="IMAGE:3060557"

(clone="IMAGE:3060557"

(clone="IMAGE:3060557"

(call_type="egrminal center B cells"

(call_line="MCGE:"

(ab_bost="DH10B (LTI)"

(note="Vector: pT773-per; Site_1: Not1; Site_2: Eco RI;

(note="Vector: pT773-per; Site_1: Not1; Site_2: Eco RI;

(note="Vector: pT773-per; Site_1: Not1; Site_2: Eco RI;

(1.5-2.5kb). Directionally cloned cytoplasmic mRNA

(1.5-2.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. and M. Bento Soares, Ph.D.

Bonaldo, Ph.D. and M. Bento Soares, Ph.D.

16 a 117 c 162 g 148 t lothers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1126
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EST 15-MAR-2000 CDNA clone

NAP./3364 SAVE BLO-acw-e-03-0-UI.81 NIH_MGC_37 Homo sapiens IMMGB:3060557 3', mRNA sequence.

AW575364.1 GI:7246903

ACCESSION VERSION KEYWORDS & SOURCE ORGANISM

AW575364

RESULT 8 AW575364/c LOCUS human. Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

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AGENCOURT 8353549 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279733 57, mRNA Sequence.
BQ706352.
BQ706352.1 GI:21845251
EST.
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Corgan: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CoNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                              1185
          1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 97)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2469 row: m column: 14
High quality sequence stop: 658.
                                                                                                                                                                       396 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAAGTGCCCCCCACCTGCTCCAGGTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                        516 GCGGTCCTCCAGCTCATTCACCTCCACCCCCCTCCTTGGCTTTAATTATGCT
                                              336 GAAACACAAAGTCTACGCCTGCGAAGTCACCCCATCAAGGCCTGAGCTCGCCCGTCACAAA
                                                                                                                                  1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG
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/db_xref="taxon:9606"
/clone="IMAGE:6279733"
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AUTHORS
TITLE
JOURNAL
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/ Observed = "Laxon: Sequences" |

/ Clone="IMAGE: 5924314" |

/ Clone="IMAGE: 5924314" |

/ Clone="IMAGE: 5924314" |

/ Lissue _ type="IJymphoma, cell line" |

/ Lissue_ type="IJymphoma, cell line" |

/ Lis
                                                                                                                                                                                                                         BQ062789 641 bp mRNA linear EST 02-APR-2002
AGENCOURT 6826785 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924314
5,, mRNA Fequence.
BQ062789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparations
CDNA Library Preparations
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information action of through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM2094 row: d column: 11
High quality sequence start: 77
High quality sequence start: 77
High quality sequence stop: 596.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 641)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT 1288
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                                    60 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT
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/organism="Homo sapiens"
/dba_tazef="axon:860"
/clone_lib="Human insulinoma"
/clone_lib="Human insulinoma"
/clone_lib="Human insulinoma"
/lab_bost="biloB (phage-resistant)"
/lab_host="biloB (phage-resistant)"
/
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Best Local Similarity 99.4'
Matches 521; Conservative
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BQ573939/c
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Emilon, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lee, Balton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Kitter, E., Ronko, I., Bennett, J., Cardens, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

Juckson, Y. and Bowers, Y.

Unpublished (2000)

Other ESTS: ihisboß x.

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Endocrine Pancreas Consortium

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Tel: 617-495-1812

Fax: 617-495-1812

Fax:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 563)
                                                                                      490 AGCAGTIGAAATCTIGGAACTGCCTCTGTTGTGTGCCTGCTGCAATAACTTCTATCCCCAGAG
                                                                                                                                                                                                                        370 TCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCA
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                                           AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGAATAACTTCTATCCCAGAG
                                                                                                                                                                                 AGGCCAAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTG
                                                                                                                                                                                                                                                                                                                   TCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGGA
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BQ573939 643 bp mRNA linear EST 19-JUN-2002 ULH-EZD-bax-d-24-0-UI.sl NC1 CGAP Chl Homo sapiens cDNA clone UI-H-EZD-bax-d-24-0-UI 3', mRNA sequence. BQ573939 I GI:21477256 EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                              301 GAAACACAAACTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA
                                                                                             CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA
                                                                                                                                                                                                                                                                                                                                                                1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                      1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAAGTGCCCCCACCTGCTCCTCAGTTCCAG
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                                                                                                                                               826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA
                                                                                                                                                                                                                     GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCCAGGAGAGTGTCACACAGAGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1186 GCGGTCCTCCAGCTCATCTTCACCTCACCCCCCTCCTTCGCTTTAATTATGCT
                                 0; Gaps
26.5%; Score 519.8; DB 13; Length 563; 99.4%; Pred. No. 1.8e-96; tive 0; Mismatches 3; Indels 0;
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source

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/note="Vector: pT713-Pac, Site 1: Not1, Site 2: Eco RI, Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento. Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AWS75927 618 bp mRNA linear EST 15-MAR-2000
UI-HF-BL0-acl-e-02-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059426 3', mRNA sequence.
                                                                                                                                                                                             1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonoclocide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                               124 GCGGTCCTCCAGCTCATTTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
( bases 1 to 618)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (LTI)"
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www.bio.llnl.gov/bbrp/image/image.html
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3059426"
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/tissue_type="lymph"
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Seg primer: Mla FORWARD
POLYA=Yes.
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TAG_IIS=UI-H-EZO
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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fclone="url-H-R20-bax-d:24-0-UI"
clone lib="NCI CGAP Ch1"
/tissue_type="Chondrosarcoma Grade II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14;
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Pred. No. 2e-96;
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Best Local Similarity 99.2%;
Matches 522; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .643
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AUTHORS
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into pT7T3-Pac vector. The oligonucleotide used to prime squence that is located between the Nort Intrary tag (dT)18 tail. The sequence tag for this library is TAG LIBEUT. +EUO TAGLOGOUNG	Local Similar Local Similar Local S20; Cor 766 AGGAAC 840 840 840 840 840 840 841 842 843 844 845 846 847 848 840 840 840 840 840	360 360 1006 300 1066 240 (09 1186 GCGGTCCTCCAGCTCTTTTTTTCCACAGGGACCTATCTTTTTTTT	AWS75346 ACCESSION ANS75346 AN
		RESULT 14 BQ181514 LOCUS LOCUS LOCUS DEFINITION UL-H-EUO-azu-i-21-0-UI.81 NCI_CGAP_CAT Homo sapiens cDNA clone ACCESSION RAGE: 5853788 3', mRNA sequence. ACCESSION BQ181514 BQ181514.1 GI:20357006 SCHNCE Numan ORGANISM Homo sapiens BURATYOCA: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Ammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS NCI-CGAP http://www.ncbi.nlm.nlm.gov/ncicgap. TILLE NGIOLE COLDE	Unpu Cont Emai Tisai Tisa CDN CDN CLON CLON CLON CLON CLON	Organism="Homo sapiens" (b) Xref="taxon:960e" (clone="lib="NOT GGAP Car!" (risue_type="Gateoarthritic Cartilage" (dev stage="Adult" Capt Car!" (fab_host="DHOB (Life Technologies)" (note="Organ: Ree; Vector: pT773-Fac (Pharmacia) with a note="Organ: Ree; Vector: pT773-Fac (Pharmacia) with a NCI CGAP Carl is a CDA library containing the following constructed according to Bonaldo, Lennon and Soare, Genome Research, 6:791-806, 1996; First strand CDNA NOt I site. Double stranded cDNA was ligated to an EcoR I site. Bouble stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally

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/organism="Homo sapiens"
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/clone="IMAGE:3060418"
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tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
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Result М О

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Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; light chain; ds; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding Humanised monoclonal antibody Hu266, light chain.
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AAS00145
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Chi220 light chain
pMDR1006 insert.
Vector pMDR1007.
Plasmid pAH4611.
pMDR986 insert. S
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Plasmid pD16hJ1.L1
                                                                                           July 18, 2003, 04:14:58; Search time 508.109 Seconds (without alignments) 8686.944 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                       2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
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Human secreted pro Human cDNA clone H

Human cDNA encodin Human breast cance Human EST-derived

pro

Human secreted

CDNA sequence #531

Human EST-derived Anti-human AILIM m

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                GATGTGGGGAGTTTATTACTGTTCTCAAAGTACACATGTTCCGTGGACGTTCGGTCAAGGC
                                                              570 AAGGAATAGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                 The invention relates a humanised antibody that specifically binds an epitope contained within positions 13-28 of amyloid beta peptide, Abeta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of toxic soluble Abeta species in humans their fragments are used for the manufacture of a medicant. This includes the prolonged expression of recombinant sequences of them in human tissues for the treatment of Clinical/pre-clinical Alzhaimer's disease, Down's syndrome or pre clinical/pre-clinical Alzhaimer's disease, Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent freverse accumulation of the Abeta sequence encodes the light chain of a humanised monoclonal antibody, Hu266, based on the mouse antibody 266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 CCACTCTCCCTGCCTGTCACCCTTGGACAACCAGCCTCCATCTCTTGCAGATCTAGTCAG 149
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/number= 1
/note= "The figure indicates that the intron
/note= "The figure indicates that the intron
finishes at nucleotide 762 but this would alter the
reading frame of the second exon and is possibly a
mistake by the authors"
741.1084
/rtag= f
/number= 2
                                                                                                                                                                                                                                                                                                                              New humanised antibody for the treatment of Alzheimer's comprises inhibition and reduction of the formation of amyloid plaques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.9%; Score 1682.8; DB 22; Length 1950; Best Local Similarity 93.2%; Pred. No. 0; Matches 1795; Conservative 0; Mismatches 122; Indels 9; C
                                                                                                                                                                                                                                                           Tsurushita
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                                                                                                                                                                                                                                                          Bales KR, Paul SM,
                                                                                                                                                                                                                                                                                                                                                              Example 13; Fig 4; 63pp; English.
                                                                                                                                                                         24-FEB-2000; 2000US-0184601.
08-DEC-2000; 2000US-0254465.
08-DEC-2000; 2000US-0254498.
                                                                                                                                                    2001WO-US06191
                                                                                                                                                                                                                                                       Holtzman DM, Demattos R,
Vasquez M;
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P-PSDB; AAU07744.
                                                                                                        WO200162801-A2
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                                                                                                                                  The sequence is that of a plasmid expressing a structurally altered BR96 antibody, having the variable region of BR96 and a modified variable region. It can be used in the production of the structurally altered antibodies which are useful for the treatment of cancer and carcinomas in vivo, especially when conjugated to cytotoxic agents. Structurally altered BR96 Ab is used, especially conjugated to doxorubicin, to treat proliferative type diseases where a cell has a BR96 antigen on the cell surface. The chimeric and humanised BR96 Ab are also used in the methods to inhibit and prevent BR96-induced toxicity resulting from immunotherapy
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           immuno:therapy - by administration of immunoglobulin fusion modified prior to administration by inactivation of part of
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8897 BP; 2410 A; 2112 C; 1967 G; 2407 T; 1 other;
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                                                                                              Disclosure; Pages 58-60; 140pp; English.
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91.9%;
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.mmunoglobulin-induced toxicity; cancer; inhibition; BR-96-induced;
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Db 1852 GGCCGTATTGAGTACTTTCCACAACCTAATTTAAT Qy	RESULT 3 AAV18693 ID AAV18693 standard; cDNA; 8897 BP. XX AC AAV18693; XX XX DT 03-AUG-1998 (first entry)		Homo sapiens. Simian virus 40 WO9805787-Al. 12-FEB-1998.	FF 01-AUG-1997; 97MO-UBL3582. XX 02-AUG-1996; 96US-0023033. XX ERIM) BRISTOL-WYERS SQUIBB CO. XX			C The sequence is that of a plasmid expressing altered BR96 antibody, having the variable r CC a modified variable region. It can be used in CC structurally altered antibodies which are use CC treatment of cancer and carcinomas in vivo, CC conjugated to cytotoxic agents. Structurally CC used, especially conjugated to doxorubicin, CC true diseases where a cell has a RP96 antiform.		Query Match 82.9%; Score 1625.8; Best Local Similarity 91.6%; Pred. No. 0; Watches 1774; Conservative 0; Mismatches	OY 33 CITAIATIGCIGCIAIGGGIAICIGGCACCIG D 1058 CIGIIGGIGCIGAIGTICIGGAITCCIGCITCCAC	Qy 93 CCAGATTCCCTGGCTGTAAGCTTAGGAGAGGGG
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2190 ACCCTTTTTCCACAGGGGACCTACCCCTATGGGGGGGATCATTCTTTCACCTCCC 2249 1215	RESULT 4 AAZ10202 ID AAZ10202 ID AAZ10202 XX AC AAZ10202; XX AC AAZ10202; XX AC AID 01-NOV-1999 (first entry) DT 01-NOV-1999 (first entry) XX XX XX XX XX Light chain variable region; chimeric anti-CD40 antibody chi22. XX XX XX Ight chain variable response; T cell dependent anti-CD40 antibody; XX
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113 GCACTGCCCAGTCCTGTCACCTTGGCATCCTTGCTTGCTT	915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCACCTACAGCCTCAGCA 974 1950 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCACCTACAGCCTCAGCA 2009 975 GTAACTCCCAGGAGAGTGTCACAGGAGAGGACAGCACCTACAGCCTCAGCA 2009 975 GCACCCTGACGCAGAGACTACGAGAAACACAAAGTCTACGCCTCCGAAGTCA 1034 2010 GCACCCTGACGCAGACAAAGACACAAACACAAAAGTCTACGCCTCCGAAGTCA 2069 1035 CCCATCAGGGCTGAGCACACACAAAAACACAAAAGTCTACGCCTCCGAAGTCA 2069 1036 CCCATCAGGGCTGAGCACACACACAAAAACACAAAAGTCTACGCCTCCGAAGTCA 1054 2070 CCCATCAGGGCTGAGCTCCCCTCACAAAAAACACCCCCCCC

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2179 ATTGCGGTCCTCCACCTCTTTCACCTCACCCCCCCTCCTCCTTCGCTTTAATTAT
                                                       .464 IGGCCATTCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCC
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Best Local Similarity 90.6%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 137; Indels 49; (
                                                                                                                                                                                                                                                                                                                     Antibody that binds human CD40, for treating T cell mediated disorders
                                                                                                                                                                                                                                                 KK, Harris LJ, Hollenbaugh Watkins JD, Wu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8858 BP; 2396 A; 2124 C; 1950 G; 2387 T; 1 other;
                                                   termination sequence"
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Huse WD, Siadak AW, Thorne BA,
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Example 2;
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                                                                                                                                                                                                                                                                                                                   complementarity determining region; humanised; chimerised; light; heavy; chain; Fq; chi220; L3.17; human; CD40; monoclonal antibody; gp39; variable; region; murine; CDR; humoral immune response; kidney; transplant rejection; anti-inflammatory; autoimmune disease; type I diabetes; psoriasis; multiple sclerosis; rhemmatoid arthritis; systemic lupus erythematosus; myasthenia gravis; inflammatory disease; T cell-dependent antigen; collagen induced arthritis; skin; ds.
                                                                                ATGITITAAGTICATGATACTIAAATGAAATGICATGCCTIATITITT
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HOLLENBAUGH
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BERRY K K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence shows the expression vector encoding the light chain of the chimerised anti-human monoclonal antibody (mAb), Chi220. Chi220 binds to human CD40 (or its active portion). It comprises murine variable and human kappa and gamma I constant regions. It binds to CD40 and effectively blocks humoral immune responses to T cell-dependent antigens in a dose dependant fashion. The antibodies of the invention are useful for modulating humoral immune responses against T cell-dependent antigens, collagen induced arthritis, and skin and kidney transplant rejection and are also useful for their anti-inflammatory properties. They are useful for treating autoimmune disease such as type I diabetes, pspriasis, multiple sclerosis, rheumatoid arthritis,
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                                                                                                                                                                                                                                                                                                                                                                              New humanized anti-human CD40 antibodies which block interaction between gp39 and CD40 for modulating humoral immune responses against T cell-dependent antigens, collagen induced arthritis, and transplant
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                                                                                                                                                                                                           Berry KK, Harris
Watkins JD;
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Pred. No. 0;
); Mismatches 137; Indels
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Wu H,
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Huse WD, V
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90.6%;
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Bajorath J,
THORNE B A.
BAJORATH J.
HUSE W D.
WU H.
                                                                                                                                         WATKINS J D.
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Matches 1783; Conserv
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1603 GGGAATCAACCAAAGCAAATTTTTCAAAAGAAACCTGCTATAAAGAAATCATTCAT	RESULT 6 AAQ30919 1D XX AC AAQ30919 TO Z-APR-1993 (first entry) XX XX Why Bubbash and pubblionsert. XX XX YX YA Plasmid; pubblionsert. XX XX YX YA Plasmid; pubblionsert. XX XX YX YA Plasmid; pubblionsert. XX	
1524 TCAGNATGGCTGCAAAAACATTTAGAACTTTATTAAGGAATAGGGG	### ### ##############################	1423 TTACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCAC 1482 2419 TTACCCTATCATCCTCTGCAAGACAGTCCTCCTCAAACCCACAAGCCTTCTGTCCTCAC 2478 1483 AGTCCCTGGGCCATGGTAGGAGACTTGCTTCCTTGTTTTCCCCTCCAGCAGCCC 1542
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isolated was ligated into NotI linearised pSAB132 which had been dephosphorylated by calf alkaline phosphatase. This generates the plasmid phymblo07. The dephosphorylated mixture was fractionated through low temperature melting agarose and used to transform E. C. 19421(Iq) to ampicillin resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3' order, the immunoglobulin kappa chain cities a period, amino acid (AA) 1-AA112 of the humanised SAB light chain variable region (LV) followed by genomic DNA encoding AA108-C. C. The polypeptide encoded by pMDR1007 is an antibody region (LC). The polypeptide encoded by pMDR1007 is an antibody complex which was shown to bind to CD4 but did not block the binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+11 lymphocytes (helper/inducer cells). The homolog blocked HIV-induced syncytia formation. This homolog can be used in the detection, prophylaxis and treatment of diseases caused by infective agents whose
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                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                           Score 1429.4; DB 13; Length 1701; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                          96; Indels
                                                                                                                                                                                                                                                                                          Sequence 1701 BP; 435 A; 468 C; 361 G; 437 T; 0 other;
                                                                                                                                                                                                                                                                                                                        Query Match 72.9%; Score 1429.4;
Best Local Similarity 93.1%; Pred. No. 0;
Matches 1534; Conservative 0; Mismatches
                                                                                                                                                                                                                                                             primary targets are CD4+ cells.
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1030 1150 1210 1224 1270 1284 1329 1344 1389 1403 1449 1463 1509 1523 1569 1629 1643 910 970 924 850 864 984 804 971 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1105 AGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC TCTGACCCTTTTTCCACAGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1271 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTG 1285 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG 1584 CTTACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAA GITACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTC TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG CTGAATAACTTCTATCCCAGAGGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGGGGATAACGCCCTCCAA TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGGACACCTACAGCCTC GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTAG AGGGAGAAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC 1330 TITIACCAACTACTCATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1524 Tricerretritricecerecreadeaaceerearageerritriaaggeraaggr CTTACAGTCATATATCCTTTGATTCCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 1510 TIGCTICCTIGITITCCCCTCCTCAGCAAGCCCTCATAGICCTTITTAAGGGTGACAGGT TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 1630 AAGAAGAACCTGCTATAAAGAGAATC 1656 aagaagaaccigcggccgarcgaric 1670 BP. standard; DNA; 1701 entry) 02-APR-1993 (first Vector pMDR1007

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The sequence given is the insert of the vector pMDR1007. pMDR1006

(see AAQ309096) and pSAB132 (see AAQ30906) were used in the construction of this vector. Three fragments were ligated together to generate this vector. Three fragments were ligated together to generate pMDR1006; a 572 bp fragment of pMDR986 (see AAQ30918) and a 326 bp Ecory(YBg111 frame). The ligation mixture was used to transform E. Coli JA221(IQ) to ampticillin resistance. pMDR1006 was transform E. Coli JA221(IQ) to ampticillin resistance. pMDR1006 was cleaved with Norl and the 1693 bp fragment isolated was ligated into Norl linearised pSAB132 which had been dephosphorylated by calf alkaline phosphatese. This generates the plasmid pMDR100? The alkaline phosphatese. This generated through low temperature melting agarcase and used to transform E. Coli JA221(IQ) to ampticillin cresistance. The pMDR1007 insert comprises DNA encoding, in a 5′ to 3′ order, the immunoglobulin kappa chain signal peptide, amino acid (AA) cresistance. The pMDR1007 insert comprises DNA encoding in a 5′ to 3′ order, the immunoglobulin kappa chain signal peptide, amino acid (AA) cresistance. The pMDR1007 insert comprises DNA encoding in a 5′ to 3′ order, the immunoglobulin kappa chain signal peptide, amino acid (AA) cresistance. The pMDR1007 insert comprises DNA encoding in a 5′ to 3′ order, the binding of gg120 (CC). The polypeptide encoded by genomic DNA encoding AA108.AA214 of the human kappa light chain, ie the light chain constant region (CC). The polypeptide encoded by DNBR1007 is an antibody homolog which was shown to bind to could but did not block the binding of gg120 to CD4. CD4 is a cell surface placed in characterior of CD4+ lymphocytes (helper/induced syncytia formation. This homolog can be used in the detection, prophylaxis and treatment of diseases caused by
Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; ECORV; pMDR986; BglI; pMDR1003; JAS21(IQ); E. Coll; ampiciallin resistance; NotI; dephosphorylate; Calf; alkaline phosphatase; low temperature; melting agarose; immunoglobulin; kappa chain; signal peptide; LC; humanised; SAB; light chain; variable region; LV; genomic; constant antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+; lymphocyte; helper; inducer; HIV; syncytia; formation; ss.
                                                                                                                                                                                            Location/Qualifiers
35..100
/*tag= a
/note= "Immunoglobulin kappa chain signal sequence"
1101..1101
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binding of HIV gp120 to CD4 but block HIV-induced syncytia
formation between CD4+ cells
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/tag= b

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/number= 1

/note= "AA1-AA112 o
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P-PSDB; AAR28809.
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                                                       13; Length 1701;
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                          Seguence 1701 BP; 435 A; 469 C; 361 G; 436 T; 0 other;
infective agents whose primary targets are CD4+ cells.
                                                                                    97;
                                                       DB
                                                    Score 1427.8;
Pred. No. 0;
0; Mismatches
                                                     Query Match
Best Local Similarity 93.1%;
Matches 1533; Conservative
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This vector was produced from the plasmid pA64270. pA64270

It is the expression vector for the light chain variable region (VL) of the antibody 128.1 which was obtained by PCR with leader/J region priming (see also AAQ43842). The vector also contains an ampicallin resistance gene, a gpt (mycophenolic acid resistance) selected marker, an immunoglobulin H ranscription of the CH gene is from the WH promoter of the chancer and an intron for V-constant region splicing.

Transcription of the CH gene is from the WH promoter of the murine 27.44 gene. The cloning of the 128.1 VL region was accomplished in two stages with the production of plasmid C pS44271 as an intermediate vector which lacks the promoter region. This plasmid was used in conjunction with pAH4602 in the production of the chimeric antibody which binds to the transferrin receptor on brain capillary endothelial cells. This antibody may be used in a conjugate in which it is linked to a neuropharmaceutical or diagnostic agent. The conjugate may be used to treat or prevent neurological disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and Alzheimers disease. It may also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14; Length 13999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody conjugates specific for transferrin receptor - used for diagnosis and treatment of cancer, AIDS and neurological
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9300..12092
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Best Local Similarity 99.5
Matches 1208; Conservative
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P-PSDB; AAR41686-87.
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                                                                                          GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTAG
                                                                                                                                                                                                              AGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC
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                                                                                                                                                                            8627 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGGAAGT
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                3327 TCTGTCCCTAACATGCCCTGTGTTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT
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                                                                                CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT
                                                                                                                       GAATAACTICTAICCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAAIC
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The sequence given is the insert of the intermediate plasmid pwDR996.

DMDR996 was constructed to carry genomic DNA encoding amino acid (AA) and the sequence but as constructed to a human kappa light chain ie. the light chain on acid (AA) to 108-AA214 of a human placental genomic DNA was prepared and cleaved with EcoR1 to give a 2.5 kb fragment. This fragment comprising the with EcoR1 to give a 2.5 kb fragment. This fragment comprising the kappa chain constant region was cloned into the EcoR1 site of puC8 to give pAB8. The DNA encoding LC was amplified from pAB8 using the primer sequences given in AAQ30194-15. The 1240 bp reaction product was ligated into EcoRV linearised pNN03 (see AAQ30565) that had been dephosphorylated. This generated plasmid pSAB153 (see AAQ30916). LC was amplified from pSAB153 using the primers given in AAQ30915 and AAQ30917 to generate an approx. 1276 bp fragment. This fragment was igated to EcoRV linearised pNN03 that had been dephosphorylated by the presence of a 1122 bp Ecol009 I restriction fragment. E. Coli GA22(14) to ampliciallin resistance. Plasmid pMNB986 was cled to transform E. Coli GA22(14) to ampliciallin resistance. Plasmid pMNB986 was used to transform E. Coli GA229, which does not methylate its own DNA. Sequence analysis of pMDR986 showed that a cloning artifact caused a NorI site 3' of the constant region to be been to replaced with a Pvul site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 TICTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGGTTTAC
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                                                                                                                                               Primer; polymerase chain reaction; PCR; amplify; intermediate; plasmid; pMp86; genomic; DMx; human; kappa; light, chain, constant; region; LC; placenta; ECORI; pUCB; pAB8; ECORV; pNN03; pSAB153; dephosphorylated; calf, alkaline phosphataee; E. coli; JA221(Iq); ECO109 I; E. coli; GM2929; mathylated; cloning artifact; NotI; PvuI; CD4; CD4; HIV; gpl20; syncytia; formation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New anti-CD4 antibody homolognes - which bind CD4, do not k
binding of HIV gp120 to CD4 but block HIV-induced syncytia
formation between CD4+ cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thomas DW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 161-2; 205pp; English
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                                                              02-APR-1993 (first entry)
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                                                                                                         pMDR986 insert.
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AAQ30918 standard; DNA; 1276

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AAQ30916 standard; DNA; 1241

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                                                                                                       TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA
                                                          204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTTCTGTC
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                                   TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC
                                                                                                                                                                                    CTTAAAACACCATCCTGTTTGCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA
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The sequence given is the insert from the intermediate plasmid pSAB153.

This plasmid was used in the construction of the intermediate plasmid pNAB986 (see AAQ30918). pWDR986 was constructed to carry genomic DNA encoding amino acid (AA) 108-AA214 of a human kappa light chain ie.

The light chain constant region (LC). Human placental genomic DNA was prepared and cleaved with ECORI to give a 2.5 kb fragment. This fragment comprains the kappa chain constant region was cloned into the ECORI site of pUCB to give pAB8. The DNA encoding LC was amplified from pAB8 using the primer sequences given in AAQ30914-15. The 1240 bp treation product was ligated into ECORY linearised plasmid pSAB153. LC was amplified from pSAB153 using the primers given in AAQ30915 and that had been dephosphorylated in This generated plasmid pSAB153. LC was amplified from pSAB153 using the primers given in AAQ30915 and caphosphorylated by calf alkaline phosphatase. The ligation mixture was used to transform E. coli JA221(Iq) to ampicillin resistance. Classic products and identified by the presence of a 1122 bp Eco0109 I restriction fragment. pWDR986 was used to transform E. coli JA221(Iq) to ampicillin resistance. Coli GN2929, which does not methylate its own DNA. Sequence analysis of pMDR986 was constant product at a cloning artifact caused a Not1 site 3' of the constant
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                                                                                                                                                                    plasmid; pMDR986; genomic; DNA; human; kappa; light; chain; constant; region; LC; placenta; EcoR1; pUC8; pAB8; EcoRV; pNN03; pSAB153; dephosphorylated; calf; alkaline phosphatase; E. coli; JA221(Iq); EcoR019 I; E. coli; GM2299; methylate; cloning artifact; Not1; Pvul; CD4; CD4; HIV; gpl20; syncytia; formation; ss.
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99.6%; Pred. No. 8.4e-268;
ive 0; Mismatches 3;
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Hybridoma producing antibody specific for interleukin-8 - used to prevent efflux of neutrophils from vasculature, and treat reperfusion injury
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Homo sapiens.
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Transgenic animal; human heterologous antibody; transgene; isotype switching; neutrophil efflux; reperfusion injury; Log binding; actoimmune reaction; inflammatory response; transplant rejection; acid induced lung injury; acute adult respiratory distress syndrome; ARDS; vasculitis; septic shock; allergic reaction; asthma; oystic fibroais; ss.

Example 42; Pages 310-312; 452pp; English.

The present sequence represents the kappa light chain plasmid, pCK7-96, which includes the kappa constant region and polyademylation site. The plasmid is used in the construction of miniganes for expression of igdkappa anti-CD4 antibodies, in the transgenic mouse of the invention. Igdkappa anti-CD4 antibodies, in the transgenic mouse of the invention. The specification describes transgenic non-human animals, especially a mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenic animals of functionally rearranging at heterologous diversity (D) gene in a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain transgene comprises at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain region gene segment are not constant region gene segment are not constant region gene segment are not constant region and so be used to prevent efflux of neutrophils from animal. The antibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and reduce itssue damage and prolong survival in animal models of acute adult respiratory discress syndrome (ARDS) and antimal models of acute adult respiratory discress syndrome (ARDS) and and induced lung influxy. The anti-IL-8 antibodies can also be used for the treatment of vasculitis, septic shock, allergic reactions

Sequence 3880 BP, 981 A; 1013 C; 921 G; 965 T; 0 other;

us-09-627-896b-21.rng

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                                                                               2554 AATTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT
                                                                                                       ACTGCAAGGTCAGAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA
                                                                                                                                                     CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT
                                                                                                                                                                                                   TITAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG
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           3880;
           Length
                                  Indels
           1044; DB 19;
No. 2.3e-235;
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0
                                  Mismatches
           Score
Pred.
                                ;
0
           53.3%;
                     Best Local Similarity 99.8
Matches 1066; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                            Ig; affinity constant; human; antigen; hybridoma; B cell; t transgenic; mouse; CD4; antibody; autoimmune; inflammatory; transplant rejection; immunoglobulin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nseq
TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG
                              3573 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composition has been developed which comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3881 BP; 981 A; 1014 C; 921 G; 965 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by transgenic mice etc.
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Pred. No. 2.3e-235;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 42; Page 260-262; 396pp; English.
                                                                                                                                                                                                                                                                                                                                                                         Kappa light chain plasmid pCK7-96
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nent of auto-immune disease
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99.8%;
                                                                                                                                                                                                  standard; DNA; 3881
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Homo sapiens.
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les 1066;
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The specification describes transgenic animals that are capable of producing a heterologous antibody. The antibodies are isolated form a hybridoma, comprising B cells, that is obtained from a transgene mouse having a genome comprising a human heavy chain transgene and a human light chain transgene. The B cells are fused to immortalized cells suitable for generating a hybridoma, which produces a detectable amount of an immunoglobulin that specifically binds digoxin or Shinga-like toxin. B cells from transgenic animals can be used to generate hybridomas expressing monoclonal high affinity human sequence antibodies. Antibodies produced from the transgenic animals of the invention can be used to treat human diseases, cancer, infectious disease, transplant rejection, blood diseases, cancer, infection disorders and other diseases. The present sequence is used in the course of the invention.
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transgenic mouse; human heavy chain transgene; digoxin;
human light chain transgene; immortalized cell; immunoglobulin;
Shinga-like toxin; autoimmune disease; cancer; infectious disease;
transplant rejection; blood disorder; coagulation disorder; ss.
                                                                                                                                                                                                                                                             heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
53.3%; Score 1044; DB 20; Length 3881;
Best Local Similarity 99.8%; Pred. No. 2.3e-235;
Matches 1066; Conservative 0; Mismatches 0; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3881 BP; 981 A; 1014 C; 921 G; 965 T; 0 other;
                                                                                                                                                                                                                                                           Novel transgenic non-human animals used to produce
                                                                                                                                                                                                                                                                                                Example 42; Page 311-313; 484pp; English.
                                                                                                                                                                                                              Ball
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                                                                                                                                                                                    (GENP-) GENPHARM INT INC.
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The present invention relates to novel transgenic nonhuman mammals, particularly rodents, comprising two human immunoglobulin (1g) loci, where one of two the human immunoglobulin loci is a human heavy chain locus and the other locus is a human light chain locus, and where one of the loci is of a transchromosome. The transgenic animals are useful for generating a number of B-cell expressing human antibody sequences. They are also useful for producing rearranged immunoglobulin sequences, producing human antibody display libraries, and generating a human sequence antibody that binds to a predetermined antigen. The produced antibodies are useful for treating immune related disorders. The present sequence represents a plasmid used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2675 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAAGAAACTCAAAAACATCAAGAT
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                                                                                                      New transgenic nonhuman mammal, useful for generating B-cells expressing human antibody sequences and generating antigen-specific hybridomas secreting human sequence antibody, comprises two human
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3881;
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Pred. No. 2.3e-235;
0; Mismatches 0;
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                                             GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC
                                                                                           TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC
                                                                                                                                                                                                                                                                                    using comparative model
                                                                                                                                                                                                                                                                                                                                NB: Humanised anti-CD18 Ab 60.3 variable light chain (pGk.11) sequences are given in Fig 10 and Sequence ID 10 of the specification; corresp. to AAQ62611 and AAQ55004 respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibody; MAb; heavy chain; light chain; constant region; variable region; amplification; primer; polymerase chain reaction; PCR; chimera; Ig; integrin; ss. immunoglobulin; humanised antibody; leucocyte; integrin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised anti-CD18 Ab 60.3 variable light chain (pGk.11).
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by computer database searching
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AAQ55004 standard; DNA; 7059 BP.
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Chimeric: Mus sp.
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These two sequences are not identical; AAQ55004 comprising 7059 bases and AAQ52611 comprising 8400 bases. Fig 10 should consist of and AAQ52611 comprising 8400 bases. Fig 10 should consist of pages 1/4, 2/4, 3/4 and 4/4), however, page 2/4 is duplicated and page 4/4 is missing. The sequence found in AAQ62611 represents pages 1/4 - 3/4.

A humanised monoclonal antibody corresponding to the murine anti-CD18 antibody 603 was prepared. The variable (V) region sequences from both the heavy (H) and light (I) chains were determined from cDNA (amplified by PCR), and spliced onto human constant (C) regions.

C camplified by PCR), and spliced onto human constant (C) regions.

C camplifing in a chimeric 60.3 Ab (1991, Kappa). The chimeric Ab was expressed in tissue culture (Ag8.653 mouse myeloma cells, detected CO by ELICBA), and examined in binding assays. The results from the Adverse competition and inhibition assays showed that the chimeric Ab was as effective as the murine 60.3 Ab. The deduced murine VH and VL protein sequences were selected to be used as and two human Ig protein sequences were selected to be used as and two human Ig protein sequences. Based on the 60.3 Fv wondel and the two human template sequences. Based on the 60.3 Fv wondel and the two competition and and the form the protein data base, and two humanised Fv was modeled. Construction of the humanised CC (spanning the entire V region) to form the VH and VL These were again compensed that the humanised Ab (1901, kappa). The humanised proteins were again competition a dozen the humanised dolls and seaved for It he humanised for It he humanised CC About a dozen of the humanised dolls and seaved for It he humanised for It he humanised cells expressing Olls and assays.
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53.1%; Score 1040.4; DB 15; Lengt.
Best Local Similarity 98.1%; Pred. No. 2e-234;
Matches 1065; Conservative 0; Mismatches 16; Indels
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4856	1069	4796	1129	4736	1189	4676	1249	4616	1309	4556	1369	4496	1429	4436	1489	4376			
4915 AAGGACAGCACCTACAGCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAA	CACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC	CACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGCC	TTCAACAGGGGAGAGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTG	TTCAACAGGGAGAGTGTTAGAGGGAGAAAGTGCCCCCACCTGCTCCTCAGTTCCAGCTG	ACCCCTCCCATCCTTTGGCCTCTGACCCTTTTCCACAGGGGACTACCCCTATTGCGG	ACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTTGTGGGG	TCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTTGGCTTTAATTATGCTAATG	TCCTCCAGCTCATTTCACCTCACCCCCCCTCCTCCTTGGCTTTAATTATGCTAATG	TTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAT	TIGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCTCTCTT	TTAATAATTATTATTATGTGTTTTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATA	TAAATAATTATTATCTGTTTTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATA	TGTAGTCATCCTAAGGCGCATAAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCT	TGTAGTCATCCTAAGGCACGTAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCT	ATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCC	ATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCC	TGGCC 1495	TGGGCC 4370	
4915	1010	4855	1070	4795	1130	4735	1190	4675	1250	4615	1310	4555	1370	4495	1430	4435	1490	4375	
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Search completed: July 18, 2003, 06:43:57. Job time : 513.109 secs

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July 18, 2003, 06:19:39; Search time 473.815 Seconds (without alignments). 8533.875 Million cell updates/sec
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1 tctagaccaccatggattca......cccacttctaggatcaattc 1960
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/cgn2_6/ptodata/1/pubpna/US10_PUBGONB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 21, Appl	Seguence 31, Appl	Sequence 1, Appli		Sequence 33, Appl	Sequence 13629, A	Sequence 81, Appl	7,	7	Sequence 7, Appli	7	53	37	Sequence 29, Appl	Sequence 79, Appl	A,
		ID	US-09-249-011A-21	US-10-027-075-31	US-10-000-433-1	US-09-954-456-771	US-09-859-053-33	US-10-198-846-13629	US-09-800-729-81	US-09-992-600A-7	US-09-924-340-7	US-10-000-489-7	US-10-000-986-7	US-09-822-830A-531	US-09-859-053-37	US-09-859-053-29	US-09-800-729-79	US-09-799-514-2
		DB	11	15	15	11	11	15	10	12	12	15	15	11	11	11	10	10
	Query	Length	1960	1708	3881	1244	948	1045	941	968	896	968	968	913	970	974	066	1033
ď	Query	Match	100.0	55.7	53.3	30.4	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.4	26.4	26.4	26.4
		Score	1960	1091.2	1044	595.8	523.4	523.4	523	523	523	523	523	522.8	518.4	518.4	518.4	518.4
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Sequence 59, Appl		Sequence 66, Appl		Sequence 57, Appl			~	•		Sequence 63, Appl	Sequence 893, App	Sequence 893, App	Sequence 893, App	Sequence 893, App	Sequence 6, Appli	Sequence 5, Appli	•	_	4		14,	9	1385	_	Sequence 1407, Ap	1407		1312
US-10-158-646-59	US-10-158-646-60	US-10-158-646-66	US-10-158-646-64	US-10-158-646-57	US-10-221-945-5	US-10-198-846-10845	US-10-158-646-63	US-10-158-646-68	US-10-198-846-14013	US-10-158-646-63	US-09-736-457-893	US-09-902-941-893	US-09-849-626-893	US-10-017-754-893	US-08-485-163-6	US-09-766-995-5	US-10-158-646-4	US-10-158-646-64	US-09-864-761-4801	US-09-292-758-57	US-09-909-567B-14	US-10-158-646-65	US-10-198-846-13859	US-09-878-178-1407	US-10-046-935-1407	US-10-146-502-1407	US-09-249-011A-7	US-10-198-846-13125
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1230	1184	1458	1775	1202	928	962	2272	853	1001	2272	477	477	477	477	1149	1149	829	1775	426	520	799	819	944	412	412	412	396	961
26.4	26.4	26.2	26.0	25.8	25.8	25.6	25.1	23.9	23.8	23.8	23.6	23.6	23.6	23.6	23.0	23.0	22.4	22.2	21.7	21.3	21.1	21.0	20.9	20.3	20.3	20.3	20.0	19.2
518.4	517.4	514.4	509.4	506.4	504.8	502	491.4	469.4	466.4	465.8	462	462	462	462	450	450	439.4	435.8	424.4	416.8	412.8	412.4	409.4	398	398	398	392.8	375.4
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ALIGNMENTS

APPLICANT: GLAMAN, SAWUEL

APPLICANT: GRAY, GARY S.

APPLICANT: KNIGHT, ANDREA

APPLICANT: NO 'HARA, DENISE

APPLICANT: NO 'BONITA

APPLICANT: NUELDMAN, GERTRUIDA M.

TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS

TITLE OF INVENTION: OF TREATHENT THEREWITH

FILE REFERENCE: 08702.0081-00000

CURRENT APPLICANTON NUMBER: US/09/249,011A

NUMBER OF SEQ ID NOS: 24

SEQ ID NOS: 24

SEQ ID NO 21

LENGTH. Gaps DB 11; Length 1960; 0 Indels . 0 Query Match
100.0%; Score 1960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1960; Conservative 0; Mismatches Application US/09249011A APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
APPLICANT: CARRENO, BEATRIZ
APPLICANT: CELNIKER, ABBIE CHERYL
APPLICANT: COLLINS, MARY
APPLICANT: GOLDMAN, SAMUEL 21, Application of US20020176855A1 ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (768)..(1087) US-09-249-011A-21 NAME/KEY: CDS LOCATION: (12)..(408) GENERAL INFORMATION: TYPE: DNA ORGANISM: Mus sp. US-09-249-011A-21 FEATURE:

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1244
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APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Hall, Ed
TITLE OF INVENTION: TRANSCHIC TRANSCHROMOSOWAL RODENTS FOR MAKING HUMAN
TITLE OF INVENTION: ANTIBODIES
FILE REPRENCE: 014643-012110US
CURRENT APPLICATION NUMBER: US,10/000,433
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/250,340
PRIOR RILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATCHIN VEr. 2.1
SEQ ID NO 1
                                                                                                    1190 GCCTGACCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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99.8%; Pred. No. 3.7e-255;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/10000433; Publication No. US20020199213A1; GENERAL INFORMATION: APPLICANT: Tomizuka, Kazuma
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACAACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTTCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTAGGAAGAAACTCCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 15; Length 1708;
                    COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FOR:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION NUMBER: US/10/027,075

FILING DATE: 20-Dec-2001

CLASSIFICATION CALASSIFICATION CALASSIFICATION CALASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 55.7%; Score 1091.2; DB 15; Lengt Best Local Similarity 99.6%; Pred. No. 2.1e-267; Matches 1115; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/227,595
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: AMP E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: «Unknown»
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-027-075-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1708 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                               GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
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                        ACTGCAAGGTCAGAAAGCATGCAAAAGCCTCAGAATGGCTGCAAAAAGAGCTCCAACAAAA
                                      2615 ACTGCAAGGTCAGAAAAGCATGCAAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAAAAAA
                                                                    2675 CAATTTAGAACTTTATTAAGGAATAGGGGAAGCTAGGAAGAACTCAAAAACATCAAGAT
                                                                                                                                TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACAACAACAAGGGGCAGAACTTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 ATCAGCAGCCTAGAGCCTGAAGATTTTTGCAGTTTATTACTGTCAACACCGTGACAA--TT
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                                                                                                                                         GENERAL INFORMATION:

JAPPLICANT: YOUNG, Paul

TITLE OF INVENTION: Sets

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR PILING DATE: 2000-09-26

PRIOR PILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR PILING DATE: 2000-09-26

PRIOR PILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,134

PRIOR PILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,710

PRIOR APPLICATION NUMBER: US/60/235,711

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27
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Pred. No. 2.8e-141;
0; Mismatches 362;
S-09-954-456-771
Sequence 771, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.4%;
Best Local Similarity 69.3%;
Matches 882; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-771
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Matches 524; Conservative
                                                                                                                                                                       LOCATION: (28)...(735)
NAME/KEY: 3'UTR
LOCATION: (739)...(948)
NAME/KEY: sig peptide
LOCATION: (28)...(87)
                                                                                                                                                                                                     ... (948)
                                                                                                                                                                                                                                         NAME/KEY: misc_feature rocation: (1)...(948)
                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                             LOCATION: (1)...(27)
NAME/KEY: CDS
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Sequence 33, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658A1uaki
APPLICANT: Hori, No. US20020102658A1uaki
APPLICANT: Hori, No. US20020102658A1uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: UF 2001-99508
                                                                                                                 612 TITIAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCT
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Pred. No. 6.7e-123;
0; Mismatches 2;
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 948
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US-10-198-846-13629
; Sequence 13629, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
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OTHER INFORMATION: n = A,T,C or G
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049 WINDER: US/10/198,846
CURRENT PELICATION NUMBER: US/10/198,846
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1045
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Facent No. US20020068319A1
GENERAL INFORMATION:
JAPLICANT:
JILLE OF INVENTION:
FILE REFERENCE: PZ044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
FRIOR APPLICATION NUMBER: PCT/US00/26013
FRIOR APPLICATION NUMBER: 60/155,709
FRIOR FILING DATE: 1999-09-24
FRIOR FILING DATE: 1999-09-24
NUMBER: OF SEQ. DI NOS: 217
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Homo sapiens
US-10-198-846-13629
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sequence 7, Application US/09992600A;
publication No. US20030027161A1
j GRERRAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
ITLEOF INVENTION: HUMAN CDNSA AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.044.D1V
CURRENT PRILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US/09/924,340
PRIOR APPLICATION NUMBER: US/09/924,340
PRIOR PRILING DATE: 2001-08-06
PRIOR PELING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-06
PRIOR PLING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-06-25
PRIOR PLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
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                                                                                                            Length 941;
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                                                                                                      tch 26.7%; Score 523; DB 10; L al Similarity 100.0%; Pred. No. 8.4e-123; 523; Conservative 0; Mismatches 0;
; SEQ ID NO 81

: LENGTH: 941

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-800-729-81
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US-09-992-600A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.7%; Scc
Best Local Similarity 100.0%; Pr
Matches 523; Conservative 0;
                   PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/
PRIOR PLILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-05-25
SOFTWARE: JPatent
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: polyA_signal
; LOCATION: 928..933
; NAME/KEY: polyA_site
; LOCATION: 953..968
US-09-924-340-7
                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: 32..748
NAME/KEY: 3'UTR
LOCATION: 749..968
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NAME/KEY: 5'UTR
LOCATION: 1..31
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US-10-000-489-7
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Publication No. US20030027248A1
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaa, Hiroaki
TITLE OF INVENTION: HUWAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERENCE: 91.US2.REG
CURRENT APPLICATION UNUBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
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100.0%; Pred. No. 8.5
:ive 0; Mismatches
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Best Local Similarity 100.(
Matches 523; Conservative
                                                                                                                                                                                                                     FEATURE:

LOCATION: 928..933

FEATURE:

FEATURE:

NAME/KEY: polya site

LOCATION: 953..968

US-09-992-600A-7
                                     TYPE: DNA
ORGANISM: Homo sapiens
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US-09-924-340-7
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Score 523; DB 12; 1
Pred. No. 8.5e-123;
); Mismatches 0;
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948 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 1007
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Sequence 7, Application US/10000986
Publication No. US20030096247A1
Publication No. US20030096247A1
APPLICANT: Benjanin, Stephane
APPLICANT: Benjanin, Stephane
FILE REFERENCE: 91.US9_DIV
CURRENT FILING DATE: 2001-11-4
FRIOR PELICATION NUMBER: US/10/000,986
CURRENT FILING DATE: 2001-11-4
FRIOR PELICATION NUMBER: US 09/924,340
FRIOR FILING DATE: 2001-08-06
FRIOR APPLICATION NUMBER: PCT/1B01/0175
FRIOR APPLICATION NUMBER: US 60/305,456
FRIOR APPLICATION NUMBER: US 60/305,456
FRIOR APPLICATION NUMBER: US 60/305,277
FRIOR PELING DATE: 2001-06-29
FRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 7
FRIONTH: 968
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Best Local Similarity 100.0%; Pred. No. 8.5e-123;
Matches 523; Conservative 0; Mismatches 0;
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| LOCATION: 1.31
| NAME/KEY: CDS
| LOCATION: 32.748
| NAME/KEY: 1919.968
| NAME/KEY: POLYA signal
| LOCATION: 928.93
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| US-10-000-986.7
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 GAACTGTGGCTGCACCATCTGTTCTTCCTCCCGCCATCTGATGAGCAGTTGAAATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAAGTGCCCCCCACCTGCTCCTCCAGTTCCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 789 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

26.7%; Score 523; DB 15; Length 968;
Best Local Similarity 100.0%; Pred. No. 8.5e-123;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps
APPLICANT: Tanaka, Hiroaki
FILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERENCE: 91.056.D19
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
FRIOR APPLICATION NUMBER: US 09/924,340
FRIOR APPLICATION NUMBER: PCT/IBO1/01715
FRIOR APPLICATION NUMBER: PCT/IBO1/01715
FRIOR APPLICATION NUMBER: US 60/305,456
FRIOR APPLICATION NUMBER: US 60/305,456
FRIOR APPLICATION NUMBER: US 60/305,277
FRIOR APPLICATION NUMBER: US 60/208,698
FRIOR APPLICATION NUMBER: US 60/298,698
FRIOR APPLICATION NUMBER: US 60/298,574
FRIOR APPLICATION NUMBER: US 60/298,574
FRIOR APPLICATION NUMBER: US 60/298,574
FRIOR FILING DATE: 2001-06-15
FRIOR APPLICATION NUMBER: US 60/293,574
FRIOR FILING DATE: 2001-06-15
FRIOR APPLICATION NUMBER: US 60/293,574
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FRIOR APPLICATION NUMBER: US 60/293,574
FRIOR FILING DATE: 2001-06-15
FRIOR APPLICATION NUMBER: US 60/293,574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..31
NAME/KEY: 5'UTR
LOCATION: 32..748
NAME/KEY: 3'UTR
LOCATION: 749..968
NAME/KEY: polyA_signal
LOCATION: 928..933
NAME/KEY: polyA_signal
LOCATION: 928..933
NAME/KEY: polyA_signal
LOCATION: 928..933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 920; NAME/KEY: PO; LOCATION: 95: US-10-000-489-7
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GENERAL INFURIALIZARI

APPLICANT: TSUJİ, TAKASHİ

APPLICANT: TSUJİ, TAKASHİ

APPLICANT: TSUJİ, TAKASHİ

APPLICANT: TSUJİ, TAKASHI

TITLE CANTI: HOLY, MONOCLONAL ANTIBODY AGAINST A

TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF

FILE REFERENCE: 06501-079001

CURRENT APPLICATION NUMBER: US/08/859,053

CURRENT FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: JP 2000-147116

PRIOR APPLICATION NUMBER: JP 2000-147116

PRIOR FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 37

"LENGHH: 970

"TENGHH: 970
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                                               808 GCGGTCCTCCAGCTCATTTCACCTCACCCCCCTCCTCCTCCTTGATTATGCT
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       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCTCCTCCTTGGCTTTAATTATGCT
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Pred. No. 1.3e-121;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/09859053; Patent No. US20020102658A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.4%;
Best Local Similarity 99.8%;
Matches 519; Conservative
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MAME/KEX: CDS
LOCATION: (33) ... (740)
NAME/KEY: 3'UTR
LOCATION: (744) ... (970)
NAME/KEY: sig_peptide
LOCATION: (33) ... (92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                                              1248 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 531, Application US/09822830A
Patent No. US20020142952A1
GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Fechtel, Kim
APPLICANT: Fechtel, Kim
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Galukota, Kamalakar
APPLICANT: Graham, James R.
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US-09-822-830A-531
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Matches 524; Conserv
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                                                         1186 GCGGTCCTCCAGCTCATTTCACCTCACCTCCTCCTTCGTTTAATTATGCT 1245
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                                                                     GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCCACCTGCTCCTCAGTTCCAG
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                                     Ouery Match
Best Local Similarity 99.8%; Pred. No. 1.3e-121;
Matches 519; Conservative 0; Mismatches 1; Indels 0;
                                                                                            1246 APIGITGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285
                                                                                                      RESULT 15
US-09-800-729-79
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                                     826 TGGAACTGCCTCTGTTGTGCCTGCTGAATAACTTCTATCCCAGAGGGCCAAAGTACA 885
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                                                0; Gaps
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26.4%; Score 518.4; DB 11; Length 974;

Best Local Similarity 99.8%; Pred. No. 1.3e-121;

Matches 519; Conservative 0; Mismatches 1; Indels 0;
                                                                      AATGTTGGAGGAATGAATAAATAAAGTGAATCTTTGCA 1285
                                                                                 899 AATGTTGGAGGAGAATGAATAAATAAAGGAATCTTTGCA 938
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OGGANISM: Homo sapiens
FERTURE:
NAME/KEY: S'UTR
NAME/KEY: CDS
NAME/KEY: CDS
NAME/KEY: 3'UTR
LOCATION: (39)...(746)
NAME/KEY: 3'UTR
LOCATION: (750)...(974)
NAME/KEY: sig_peptide
LOCATION: (39)...(104)
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-04-353-393
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US-09-301-593-27
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US-09-049-672A-19
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Maximum Match 100%
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ALIGNMENTS

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1122 TCTCTTTCCTGCAGGCCCAGCCAGTATTAGC---------GACTACTTA 1163
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                                                                                APPLICANT: Atulfo, Alejandro A.
APPLICANT: Siadak, Anthony W.
APPLICANT: Siadak, Anthony W.
APPLICANT: Barris, Linda
APPLICANT: Harris, Linda
APPLICANT: Harris, Usurgen
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
FILE REPERBNCE: DEZA SEQUENCE
CURRENT APPLICATION NUMBER: US/09/247,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1611.8; DB 4;
Pred. No. 0;
0; Mismatches 137;
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EARLIER APPLICATION WUMBER: 09/026,291
EARLIER FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 8858
Sequence 6, Application US/09247352
Patent No. 6312693
GENERAL INFORMATION:
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ilarity 90.6%;
Conservative (
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Matches 1783; Conserv
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68

Sequence

US-08-457-918-11

0 0 0 0 0 0 0 0 0 0	RESULT 3 US-07-916-098A-54 US-07-916-098A-54 Sequence 54, Application US/07916098A Sequence 54, Application US/07916098A Sequence 54, Application US/07916098A Sequence 54, Application US/07916098A Separatr Beneral Information: Separatr Beneral Index Defent D. APPLICANT: THOMAS, DAVID W. APPLICANT: THOMAS, DAVID W. ITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION ITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION CORRESPONDENCE 61 CORRESPONDENCE ADDRESS: ADDRESSEE: ALEGRETI & WITCOFF, LTD. STREET: 10 SOUTH WACKER DRIVE CITY: CHICAGO
0.0000ACATTGTGCTGACACTCTCCAGATTCCCTGGCTGTAACTTAGGAGAGAGA	883 ACAGTGGAAGGTGGATAACGCCTCCAATCGGGTAACTCCCAGGAGGGGGGGG

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----TTCTAAACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAG
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1285 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG
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TCGACGTTCGGTCGAAGGACAAGCTGGAAATCAAACGTAAGTGAACT-------- 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.9%; Score 1429.4; DB 2; Length Best Local Similarity 93.1%; Pred. No. 0; Matches 1534; Conservative 0; Mismatches 96; Indels
STATE: ILLINOIS

COUNTRY: U.S.A.

ZIP 66060

ZORPICE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTANE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: U1/2 4, 1992
CLASSIFICATION NUMBER: 27, 1991
CLASSIFICATION NUMBER: 27, 1991
CLASSIFICATION 424
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION NUMBER: 27, 1990
CLASSIFICATION NUMBER: 26,949
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION NUMBER: 26,949
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION NUMBER: 26,949
FILING DATE: JONNELL.
RESTERNICE/DOCKET NUMBER: 92,310-G
TELEFRAX: (312) 715-1234
TELECOMMUNICATION INFORMATION:
TELEFRAX: (312) 715-1234
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                                                                                                              /note= "pMDR1007 inser
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Best Local Similarity 93.13
Matches 1534; Conservative
                                                                     misc_feature
                     FEATURE:
NAME/KEY: misc_featu
LOCATION: 1
LOCATION: 1
OTHER INFORMATION: /
OTHER INFORMATION: /
FEATURE:
NAME/KEY: exon
LOCATION: 35.436
FEATURE:
NAME/KEY: exon
LOCATION: 35.436
FEATURE:
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782..1101
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; LOCATION:
US-07-916-098A-55
          NAME/KEY:
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US-07-916-098A-55
US-07-916-098A-55
Sequence 55, Application US/07916098A
Sequence 55, Application US/07916098A
Sequence 56, Application US/07916098A
Setent No. 5871732
GENERAL INFORMATION:
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: ALLEGRETTI & WITCOFF, LTD.
                                                                                                              1584 CTTACGGTCATATACTCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAA 1643
1510 TIGCTICCTIGITITCCCCTCCTCAGCCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT
                                1524 TIGCTICCTIGTITICCCCTCCTCAGCAAGCCCTCATATTTAAAGGGTGACAGGT
                                                                                      CTTACAGTCATATACCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08643
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION NUMBER: 07/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
APPLICATION NUMBER: 05,6949
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
                                                                                                                                                                                                               1644 AAGAAGAAACCTGCGGCCGATCGATTC 1670
                                                                                                                                                                  AAGAAGAAACCTGCTATAAAGAGAATC 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 10 SOUTH WACKER DRIVE CITY: CHICAGO STATE: ILLINGTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
join(101..437, 782..1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60606
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92,310-G
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/
FILING DATE: July 24, 1992
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TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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FEATURE:
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LOCATION:
FEATURE:
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FEATURE:
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Miltia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPALIDLE
OMPOTER: TBM PC COMPALIDLE
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APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-000-1991
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-000-1991
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 26-000-1991
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1990
ATTORNEY/AGBRIT NUPORAMITON:
APPLICATION NUMBER: US 07/404,089
ATTORNEY/AGBRIT NUPORAMITON:
AMADER: 07-SEP-1989
ATTORNEY/AGBRIT NUPORAMITON:
AMADER: 07-SEP-1989
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LOCATION: 1.1399
OTHER INFORMATION: /note= "Function = "Expression
OTHER INFORMATION: Vector Coding Sequence""
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                   TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCCTG 850
                                                                          CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 910
                                                                                        TCGGGTAACTCCCAGGAGAGTGTCACAGAGGACAGCAAGGACAGCACCTACAGCCTC 970
                                                                                                                                                TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAAGGACAGCAAGGACAGCTACAGCCTC 984
                                          805 TTCATCTTCCCGCCATCTGATGAGCAGTTGAATCTGGAACTGCCTCTGTTGTTGTTGTGG
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10.08-44-644-24
1 Sequence 24, Application US/08444644
1 Sequence 24, Application US/08444644
1 Patent No. 6015555
1 FALCANT FIXED.
1 TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
1 TITLE OF INVENTION: ANTIADDY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
1 TITLE OF INVENTION: CONJUGATES
1 NUMBER OF SEQUENCES: 46
1 CORRESPONÇENCE ADDRESS:
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ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ilarity 99.5%;
Conservative 0
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LENGTH: 13999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 1..13999
OTHER INFORMATION: /not
OTHER INFORMATION: Vect
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 1208, Conserv
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            733 TACTTAAACACCATCCTGTTTGCT
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US-08-232-246A-24

Sequence 24, Application US/08232246A

Sequence 10. Sequence 24, Application US/08232246A

PATENT NOTEMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

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                                                                                        P. C.
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Vector Coding Sequence""
                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,246A
FILING DATE: 04-MAY-1994
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESSPONDENCE ADDRESS:
ADDRESSPEE: Hamilton, Brook, Smith & Reynolds,
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1184.2; DB 4
Pred. No. 2.1e-298;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-MAY-1994
CLASSIPTICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE, DOCKET NUMBER: ALK88-15AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   613
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APPLICANT: CHISHOLM, PATRICTA L.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, WARGARET D.
TITLE OF INVENTION: ANTI-CHAMIST OF ALDS, ARC AND HIV INFECTION
WHITE OF STRUKTORS:
COMPRESS CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. CONTROL D. 
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60.3%; Score 1181.4; DB 2; Length 1276;
Best Local Similarity 98.9%; Pred. No. 3.9e-298;
Matches 1210; Conservative 0; Mismatches 11; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1 _ OTHER INFORMATION: /note= "pMDR986 insert"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 973 CAGCACCCTGACGCTGAGCAAGCAGACTACCAGAAACACAAAGTCTACGCCTGCGAAGT 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1032 | 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTAACTCCCAGGAGAGTGTCACAGAGGACAGGAAGGACAGCACCTACAGCACCTCAG 8626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8807 IGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCTTTCACCTC 8866
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                                                                                                                                                                                                                                                                                                                                                               TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
                     3327 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCCAAGGGCAGAACTTTGT 8386
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                                                                                                                                                                                                     CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
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                                                                                TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT
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S-07-916-098A-53 Sequence 53, Application US/07916098A Patent No. 2871732 GENERAL INFORMATION: APPLICANT: BURKLY, LINDA C.

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APPLICANT: BURKLY, LINDA C.

APPLICANT: CHISHOLM, PATRICIA L.

APPLICANT: THOWAS, DAVID W.

APPLICANT: ROSA, WARGARET D.

APPLICANT: ROSA, WARGARET J.

APPLICANT: ROSA, JOSEPH J.

APPLICANT: ROSA, JOSEPH J.

TITLE OF INVENTION: ANTI-CD4 ANTIBODY, HOMOLOGS USEFUL IN

TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 TICIABACTCTGAGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCATION: 1 - LOCATION: 1 - COTHER INFORMATION: /note= "pSAB153 insert"
US-07-916-098A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSILCATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/08843

FILING DATE: No. 5871732ember 27, 199
CLASSIFICATION: 424

APPLICATION WUMBER: 07/618,542

FILING DATE: No. 5871732ember 27, 199
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL

REGISTRATION.NUMBER: 26,949

REFERENCE/DOCKET NUMBER: 92,310-G

TELEPHONE: (312) 715-1000

TELEPHONE: (312) 715-1000

TELEPHONE: (312) 715-1234

TELEPHONE: 910/221-5317

INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                      E: ALLEGRETTI & WITCOFF, LTD
10 SOUTH WACKER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                     STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                   BURKLY, LINDA C.
CHISHOLM, PATRICIA
THOMAS, DAVID W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
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Best Local Similarity 99.6
Matches 1205; Conservative
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EDNESS: single
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SOFTWARE: WORD PE
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STRANDEDNESS:
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                            264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACAACACCCAAGGGCAGAACTTTGTTA
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615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC

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RESULT 8 US-07-916-098A-51 Sequence 51, Application US/07916098A ; Patent No. 5871732

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CAGGAACTGTGGCTGCACCATCTGTCTTCCTTCCCGCCATCTGATGAGCAGTTGAAAT
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Sequence 31, Application US/09227595
Patent No. 6444792
GENERAL INFORMATION:
APPLICAMT: Gray, Gary, Gary S. et al.
TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
TITLE OF INVENTION: Having Modified Effector Functions and Uses INVENTER OF SEQUENCES: A STREET OF SEQUENCES: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CLTY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.7%; Score 1091.2; DB 4; Length 1708; Best Local Similarity 99.6%; Pred. No. 1.4e-274; Matches 1115; Conservative 0; Mismatches 3; Indels 2;
                                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                             ZIP: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,595
                                                                                                                                                                                                                                                                                                                                           FILTING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/595,590
ATTORNEY AGENT INFORMATION:
NAME: Amy E. Mandragoura's
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
RELEPAX: (617)227-5941
INPORMATION POR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1708 base pairs
TYPE: NULCIPIC acid
STRANDEDNESS: single
                                                                                                                                                                Boston
: Massachusetts
RY: USA
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US-09-227-595-31
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                                                             264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACAACCACCCAAGGGCAGAACTTTGTTA 323
                                                                                                                         CTTAAACACCATCCTGTTTGCTTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 383
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     TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 263
                                                                                                   CITAAACACCAICCIGIIIIGCIICIIIICCICAGGAACIGIGGCIGCACCAICIGICIICA 794
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                                       TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCCAAGGGCCAGAACTTTGTTA
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433 AATICIAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT
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Pred. No. 3.8e-262;
0; Mismatches 0;
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FILING DATE: 10-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTOMBEY APPLICATION NUMBER: WO PCT/US97/21803
ATTOMBEY APPLICATION NUMBER: MO PCT/US97/21803
ATTOMBEY APPLICATION NUMBER: MO PCT/US97/21803
ATTOMBEY APPLICATION NUMBER: MO PCT/US97/21803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICKATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699.
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
APPLICATION NUMBER: US 08/352,322
                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION TO APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/352,322 FILING DATE: 07-DEC-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/544,404 FILING DATE: 10-OCT-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36,429
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 36
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Best Local Similarity 99.8
Matches 1066; Conservative
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STRANDEDNESS: sing
     FILING DATE: 13 CLASSIFICATION:
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945 ACAGCAAGGACAGCACCTACAGCTCAGCAGCACCCTGACGCAAAGCAGACTACG
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BATERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1604 GGAATCAACCAAAGCAAATTTTTCAAAAGAAAGAAACCTGC 1643
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COMPUTER READABLE FORM;

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
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Center, Eighth Floor
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STREET: TWO Embarcadero Ce
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-042-353-369
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433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT
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Sequence 217, Application US/08758417A
Patent No. 5300129
GENERAL INFORMATION:
GENERAL LONDERG, Nils
RAY, ROBER M
TITLE OF INVENTION:
Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3881;
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER CALIFORNIA

COUNTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BEN PC compatible

COMPUTER: BEN PC compatible

CORPUTER: BEN PC compatible

CURRENT APPLICATION NUMBER: US/08/758,417A

FILING DATE: US-0CT-1996

APPLICATION NUMBER: US 08/25,417A

FILING DATE: US-0CT-1996

APPLICATION NUMBER: US 08/54,404

FILING DATE: 10-0CT-1996

APPLICATION NUMBER: US 08/35,322

FILING DATE: US-0CT-1996

APPLICATION NUMBER: US 08/35,322

FILING DATE: US-0CT-1994

APPLICATION NUMBER: US 08/16,699

FILING DATE: US-DEC-1994

APPLICATION NUMBER: US 08/16,739

FILING DATE: US-DEC-1993

APPLICATION NUMBER: US 08/16,739

FILING DATE: US-DEC-1993

APPLICATION NUMBER: US 08/16,762

FILING DATE: 18-0V-1993

APPLICATION NUMBER: US 08/05,762

FILING DATE: 18-0V-1993

APPLICATION NUMBER: US 08/05,762

FILING DATE: 22-JUL-1993

APPLICATION NUMBER: US 08/05,762

FILING DATE: 22-JUL-1993

APPLICATION NUMBER: US 08/053,131

FILING DATE: 22-JUL-1993

APPLICATION NUMBER: US 08/053,131

FILING DATE: 22-JUL-1993

APPLICATION NUMBER: US 08/053,131

FILING DATE: 18-DEC-1992

APPLICATION NUMBER: US 08/155,301

FILING DATE: 18-DEC-1993

APPLICATION NUMBER: US 08/053,131

FILING DATE: 18-DEC-1993

APPLICATION NUMBER: US 08/053,131

FILING DATE: 18-DEC-1993

APPLICATION NUMBER: US 08/053,131

FILING DATE: 18-DEC-1993

APPLICATION NUMBER: US 08/050,762

FILING DATE: 18-DEC-1993

APPLICATION NUMBER: US 08/050,762

FILING DATE: 18-DEC-1993

APPLICATION NUMBER: US 08/050,762

ATTORNEY/ASANATION: 13-03
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                                                                                                                                                                                                                                                                    LLP
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: STEALILLY, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGU
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99.8%; Pred. No. 3.8e-262;
tive 0; Mismatches 0;
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MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-08-758-417A-217
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STRANDEDNESS: single
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 417
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Matches 1066; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3395 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATTATTG-T 3453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3454 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCCTAAGGGCGCATA 3513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2735 TITAAATACGCTTCTTGGTCTCCTTGCTAAATTATCTGGGATAAGCATGCTGTTTTCTG 2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGGACACCTACAGCCTCAG 3094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAAGTCTACGCCTGCGAAGT 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGACCCTTTTTCCACAGGGGACCTACCCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATC 3034
      2555 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614
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                                                                                                          2615 ACTGCAAGGTCAGAAAAGCATGCAAAAGCCCTCAGAATGGCTGCAAAAAGGCCTCCAACAAAA
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                                                               ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAAAGAGCTCCAACAAAA
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Transgenic No. 6255458-Human Animals for
Producing Heterologous Antibodies
421
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   TITLE OF INVENTION: Transgenic No. 6255458-Humar VITLE OF INVENTION: Producing Heterologous Antit NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
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PRIOR APPLICATION DATA:
APPLICATION APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION BATA:
APPLICATION DATA:
APPLICATION UNDER: US 07/810,279
FILING DATE: 10-DEC-1991
PRIOR APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
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PRING DATE: 03-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/165,699

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/209,741

FILING DATE: 09-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/352,322

FILING DATE: 07-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/544,404

FILING DATE: 10-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/544,404

FILING DATE: 10-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463

FILING DATE: 10-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463

FILING DATE: 10-OCT-1995

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APPLICATION NUMBER: US 08/728,463

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APPLICATION NUMBER: US 08/728,463

FILING DATE: 10-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096 777
FILING DATE:
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FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/09/042,353
13-MAR-1998
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMOPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   94111-3834
                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG
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; Sequence 393, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
                                                                                                                                                                                                                                              2735
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REGISTRATION NUMBER: 36,429
ERERENG/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

NAME: Apple, Randolph T

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Query Match
Best Local S
Matches 732
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                                                                                                                                                                         Length 3819;
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                                                                                                                                                                 Ouery Match 36.2%; Score 709.4; DB 4; Best Local Similarity 99.6%; Pred. No. 4.9e-175; Matches 732; Conservative 0; Mismatches 1;
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US-08-758-417A-243
; Sequencé 243, Application US/08758417A
; Patent NO. 6300129
; GENERAL INPORMATION:
APPLICANT: Lonberg, Nils
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TELEFAX: (415) 576-0300
INFORMATION FOR EGO ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3819 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                   ; TOPOLOGY: linear; ; MOLECULE TYPE: DNA US-09-042-353-393
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Kay, Robert M. Transgenic No. 6300129-Human Animals for PINVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: FIDORY disk
COMPUTER: HBM PC compatible
COMPUTER: HBM PC compatible
COMPUTER: HBM PC compatible
COMPUTER: HBM PC compatible
COMPUTER: HBM PC compatible
COMPUTER: HBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30

RESTRICATION NUMBER: US/08/758,417A

FILING DATE: 10-0CT-1996
FILING DATE: 10-0CT-1996
FILING DATE: 10-0CT-1996
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/252,322
RPELING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/155,301
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/155,313
APPLICATION NUMBER: US 08/155,313
APPLICATION NUMBER: US 08/155,313
APPLICATION NUMBER: US 08/155,313
APPLICATION NUMBER: US 08/155,313
APPLICATION NUMBER: US 08/155,313
APPLICATION NUMBER: US 08/155,131
APPLICATION NUMBER: US 08/155,313
APPLICATION NUMBER: US 08/155,313
APPLICATION NUMBER: US 08/155,313
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                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew Lip
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUWRY: USA
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REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEBHOKE: (415) 576-0200
TELEFAX: (415) 576-0300
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Pred. No. 4.9e-175;
0; Mismatches 1;
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INFORMATION FOR SEQ ID NO:
                                                                                                 NUMBER OF SEQUENCES:
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APPLICANT: Park, John E.
APPLICANT: Bamberger, Uwe
APPLICANT: Bamberger, Uwe
APPLICANT: Bamberger, Uwe
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Retrig, Wolfgang J.
ITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
ITLE OF INVENTION: PAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.189001
CURRENT PELLING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-04-30
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 8068
                  GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAACTGCCCCCCACCTGCTCCTCCAGTTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-3101-593-27
Sequence 27, Application US/09301593A
Patent No. 6455677
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| APPLICANT: Garin-Chesa, Pilar |
| APPLICANT: Garin-Chesa, Pilar |
| APPLICANT: Bamberger, Uwe |
| APPLICANT: Leger, Oliver |
| APPLICANT: Saldamha, Jose W. |
| APPLICANT: Saldamha, Jose W. |
| APPLICANT: Retlig, Wolfgang Ji. |
| TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility |
| TITLE REFERENCE: 0652.1890001 |
| CURRENT APPLICATION NUMBER: EP 98107925.4 |
| EARLIER PAPLICATION NUMBER: EP 98107925.4 |
| EARLIER PAPLICATION NUMBER: US 60/086,049 |
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| FARLIER PAPLICATION NUMBER: US 60/086,049 |
| SARLIER APPLICATION NU
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 10397.705 Million cell updates/sec 1 tctagaccaccatgggttgg.......2cggggtaaatgagtgaattc 2249 4109280 5.1.6 Compugen Ltd. Total number of hits satisfying chosen parameters: 2054640 segs, 14551402878 residues GenCore version Copyright (c) 1993 - 2003 Minimum Match 0% Maximum Match 100% Listing first 45 summaries nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-09-627-896B-23 2249 9b_par: *
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Database

1 (bases 1 to 2560)
Burkly, L.C., Chisholm, P.L., Thomas, D.W., Rosa, M.D. and Rosa, J.J.
Burkly, Anti-Cdy antibody homologs useful in prophylaxis and treatment of
AIDS, ARC and HIV infection
Patent: US 5871732-A 44 16-FEB-1999; 2560 bp Sequence 44 from patent US 5871732. AR035228 AR035228.1 GI:5951896 Unknown. Unclassified. Unknown. RESULT 1
AR035228
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL

Pred. No. is the number of results predicted by chance to have a

em_htgo_mus: * em_htgo_other: *

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Submitted (07-OCT-1999) Hougs L., Dept. of Clinical Immunology,
sect. 7631, National University Hoppital, Rigshospitalet, Tagensvej
20, DK-2200 Copenhagen N., DENNARR
Related sequences Z49801 and Z49802.
Location/Qualifiers
1. 2010
/organism="Homo sapiens"
                                                                                                                                                    2166
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The first constant-domain (CH1) exon of human IGHG2 is polymorphic and in strong linkage disequilibrium with the CH2 exon polymorphism encoding the G2m(n+) allotype in Caucasians

Immunogenetics 52 (3-4), 242-248 (2001)
                                      2104
                                                                            2106
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                                                                                                                                                                               TUCTICCTCTACAGCAGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTC 2224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AJ250170.1 GI:10799663
Constant region; IgG2 gene; immunoglobulin; immunoglobulin heavy
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AGCCTGACCTGGCTCGAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCC
                                   2045 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATGGCCGTGGAGTGGGAGG
                                                                          AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ellison, J. and Hood, L.
Linkage and sequence homology of two human immunoglobulin pheavy chain constant region genes
Proc. Natl. Acad. Sci. U.S.A. 79 (6), 1984-1988 (1982)
82197621
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/cell_type="lymphocytes"
/tissue_type="blood"
/country="Denmark"
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db_xref="taxon:9606"
chromosome="14"
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clone="pigG2n+1"
haplotype="G2m(n+)"
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216. .1803
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On Mar 2, 2000 this sequence version replaced gi:32759.
[2] also reports sequences for gamma-1, gamma-4, and a gamma pseudogene. Most of this sequence is 95% homologous with gamma-4. The hinge exons are only 70% homologous. The authors estimate that gamma-2 and gamma-4 are settled to the interpretation of the authors in important role in the evolution of human gamma genes. They also report the hinge regions of gamma-1, gamma-4, and a genes to be between 7.7 and 4.4 million years ago. This entry is part of a multigene region containing the gamma-2, gamma-4, and epslion-1, and alpha-2 genes. The relative locations of the four genes were determined by Flanagan and Rabbitts (Nature 300, 709-713
ATGACCAAGAACCAGGTCAGCCTGACCTGC 1998
                                                                                                  GCCGTGGAGTGGGAGCAATGGGCAGCCG 2058
                                                                                                                                                                                                        CTGGACTCCGACGGCTCTTCTTCCTCTAC 2118
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linkage of the gamma 2 and gamma 4
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Nikaido,T., Nakai,S. and Honjo,T.
n gamma genes: implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aniata, Vertebrata, Euteleostomi,
tarrhini, Hominidae, Homo.
937)
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480. 1802
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/gene="IgH"
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'gene="IgH"
                                                                    gene="IgH"
479. .1799
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RECPPCPAPVAGESYFLPPPKPKOTHM SRTPSVTCVVVDVSHEDPBYQFNWYVDGY
VGNARKTKPREGFNSTFRVUSVLTVVHQDMLNGKEYKCKVSNKGLPAPIEKTISKTK
SQPREPQVYTLPPSREMTRNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPML
SGGSFFLXSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK"
                                                                                                                                                                                                                                                                                                                                                                             translation="STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA
(1982)). They refer to this gene group as region B. The region A genes are gamma-1, pseudo-epsilon, alpha-1. Flanagan and Rabbits also determined the general locations of the two regions. They place region A between the JH/mu/dalta region and region B. Human fetal liver DNA, library of T. Maniatis [3] and Lawn et al [2], [1]; clones p-gamma-2RPA3 [2], 5A [3], and Ig-gamma-2-15 [1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="immunoglobulin heavy chain constant region CH1"
10. 901
gene="IgH"
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"gene="1gH"

"oin(<216. .509,902. .937,1056. .1382,1480. .1802)

"gene="1gH"

"codon start=3

"product="immunoglobulin gamma-2 heavy chain"

"prochi.id="AABS9393.1"

"db_xref="GI:184758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="immunoglobulin heavy chain hinge"
                                                                                                                                       organism="Homo sapiens"
db_xref="taxon:9606"
map="14q32.33"
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/gene="IgH"
/note=="G00-119-338"
/gene="IgH"
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/gene="IgH"
/note="IGHG2"
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                      TCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGGGGGCCCTGGGCTGCCTGG
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                        Center clone name: 815_P.21
Sequencing vector: Plasmid; n/s; 100% of reads
Sequencing vector: Plasmid; n/s; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 55130 bases at least Q40
Consensus quality: 55680 bases at least Q30
Consensus quality: 56050 bases at least Q20
Insert size: 61000; agarose-fp
Insert size: 56110; sum-of-contigs
Quality coverage: 7.9 in Q20 bases; sum-of-contigs
Quality coverage: 8.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 56310;
                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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46567 4666: gap of 100 bp
46667 50756: contig of 4090 bp in length
50857 56310: contig of 5454 bp in length.
Location/Qualifiers
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Pred. No. 0;
0; Mismatches
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A.F.A. & Green, P. (1996-1997)
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/note="assembly_fragment
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/db_xref="taxon:9606"
/clone="RP11-815P21"
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                                                                                Center code: WIBR
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Best Local Similarity 98.9%;
Matches 1787; Conservative
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/db_xref="GI:14030849" /translation="EVXLQZSGTVLARPGASVRMSCKASG Lbw.IGGTYPORNETRYTOR.RCMASTATARATYANELS YADFINDYMGGGTTVYYORRDTYTORSTORALTARATYANELS YADFINDYWGGGTTVYYSTASTKGPSVPELACSSTSTES SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFTOTO VERKCVCPEPPPRAGPSVAGPSVPELPPRKRDTMJNSRTPE WYDDGTVHNAKTKPREEDFRFPRYSCYTUVHODULNG TISKTKGOPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP TYPPMLDSDGSFPLYSKLTVDKSRWQGGNVFSCSVMHEAL 1 . 364 AO1 . 1364 AO1 . 1218 AO1 . 1663 AO1 . 1663 AO1 . 1663 AO1 . 1663 AO1 . 1061 . 2083	Score 1752.8; DB 9; Pred No. 0; Mismatches 109; GGGGTGGGGTGAAGGCC GGGATGGGTGAAGGCC GGGATTGACTGGCTAGGCCAAGCCCAACGCAAGCCAAGC	190	310 IGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAA	Db 362 CAGGTGAGTGC	Oy 595 CTGCGCCTGGGCCCAGCTCTGTCCCACCGCGGTCACATGGCACCACCTCTTGCAG 654 137 CTGCGCCCTGGGCCCAGCTCTGTCCCACCGCGCATGGCACCACCTCTTGCAG 496 638 CTCCACCAGGGCCCAGCTCTGTCCCCCTGGCGCCTCCAGGACCTCTTTGCAG 496 Oy 658 CTCCACCAGGGCCCATCGGTCTTCCCCTTGGCGCCTCCAGGAGCACTCTCTTGCAG 114 19
	2059 GAGAACAACTACAAGAACCACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTCT 2118	2239 5447 AF	AF237584 AF237584.1 GI:9857754 Homo sapiens. Homo sapiens Homo sapiens Homo sapiens Chordata, Craniata, Vertebrata, Eute Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Hom 1 (bases 1 to 2193) Vidarsson,G., van der Pol,W.L., van den Elsen,J.M.H., Vi Jansen,M., Duljs,J., Morton,H.C., Boel,B., Daha,M.R., Co and van de Winkel,J.G.J.	Activity of human 1gG and 1gA subclasses in immune defense again Neisseria meningliidis serogroup B U. Immunol. 166 (10), 6250-6256 (2001) 21240682 (2002) 2142668 (2003) 2142648 (2003) 21039264	Medical Center Utrecht, Rm. KC.02-085.2, Lundlaan 6, Ut EA, The Netherlands Location/Qualifiers (-1.219) 1.1.219 1.2.219 1.2.2
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Qy 1855 AGAGGCCGGCTCGGCCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCT 1914 bb 1697 AGAGGCCGGCTCGGCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCT 1756 Qy 1915 ACAGGGCAGCACCCACCTCTGCCCTGCCCCATCCCGGGAGGATGACC 1816 Qy 1975 ACAGGGCAGCCCCGAGAACCACAGGTGACACCTCCCCGGGAGGAGATGACC 1816 Qy 1975 ACAGGGCAGCCCGAGAACCACAGGTGAACACCTCCCCGGGAGGAGATCGCCGTG 1876 Qy 2035 GAGTGGGCAGCTGACCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTG 1876 Qy 2035 GAGTGGGAACCAGGCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTG 1876 Qy 2035 GAGTGGGAACCAGGCTGGCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTG 1876 Qy 2035 GAGTGGGAACCAGGCAGAACAACACACACCACCCCCATCGCGGACACCTCCCAGGACACACCTCCCCATGCTGGACAACACCACCTCCCATGCTGGACAACACACAC	RESULT 6	Query Match 73.4%; Score 1651.6; DB 6; Length 2287; Best Local Similarity 87.2%; Pred; No. 38-311; Matches 1998; Conservative 0; Mismatches 219; Indels 75; Gaps 14; Qy 6 ACCACCATGGACTGAACTTATCATCTTTTGTGTGCACAGCTACAGGTTC 62 Db 7 ACCACCATGGACTGAACTTCATTTTTTTTTTTTTTTTTT
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Unclassified.

(bases 1 to 2287)
Seed, B. and Walz, G.
Nucleic acid encoding an antibody that inhibits cell adhesion protein-carbohydrate interactions
Patent: US 5801044-A 1 01-SEP-1998;
Location/Qualifiers
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Pred. No. 3e-311;
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63 CACTCCCAGGTCCAGCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG 122	243 AACTACAACCAGAAGTTTAAGGCAAGGCACAATGACTGTAGACAAGTCGACGACCACA 30 247 AACTACGCAGAAGTTCCAGGGCAAGGCACAATGACGACGACACA 30 303 GCCTATATGGAACTTCTTGAGAACTCTCAAGGATACGCCGGACAATTACCACGACACACA 30 307 GCCTACATGGACTTAGTTCTTTGAGATCTCAAGGATACGCCGTTTATTACTGTGCAAGA 36 307 GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACCACGGCCGTGTATTACTGTGCGAGA 36	363 367 390 427	450 GCGAGCCGGGCCTGACTTTGGGCTAGGGAGGGGGCTAAGGTGAGGCAGGTGGCG 509	1	7150750750	895 930 955 990 1014 1050	
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1906 CCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGT - CCTACAGGGCAGCCCCGAGAA 1964 1933 CCACAGGTGTACACCCTGCCCCATCCGGGGAGATGACCAAGAACCAGGTCAGCTG 1992	2085 CAGCCGGAGAACTACAAGACCACCCTCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTCTTCTCTTGTTCTTAGAGAGAG	Db 2205 TCCGTGATGCATGAGCTCTGCACAACCACTACAGGAAAGAGCTCTCCCTGTCTCCG 2264 Qy 2233 GGTAAATGAGTG 2244 Db 2265 GGTAAATGAGTG 2276		COMMENT OS Underfulled NICLASSIFIED REFERENCE 1 (bases 1 to 2287) AUTHORS Brian, S. and Gazdy, AUTHORS Antibody capable of being used for inhibition of interaction JOURNAL Patent: JP 2000325092-A 1 28-NOV-2000; COMMENT OS Unidentified PU SO00325092-A/1	PU 28-NOV-2000 UP 2000102880 PR 04-ARK-2000 UP 2000102880 PR 23-MOV-1990 US 07/618314 PI SHEED BRIAN WARTZ GARD PC C12N15/09, A61X39/395, A61F9/10, A61P17/06, A61P29/00, A61P29/00, C7 C07X16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, G01N33/53, PC C7X16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, G01N33/53, PC C7 Strandedness: Single, CC Strandedness: Single, FH Key Linear; FH Key Location/Qualifiers FT source 1.2287	ATURES ATURES Location/Qualifiers source 12287 Advantam="unidentified" Advard="taxon:32644" Advard="taxon:32644" Advard="taxon:32644" Advard="taxon:32644" SE COUNT 478 a	DB 7 ACCACCATGGACCTGGAGGTTCCTCTTTGTGGTGGCACCAGCTACAGGTGTC 66

	RESULT 9 190051	Query Match 73.4%; Score 1651.6; DB 6; Length 2287; Best Local Similarity 87.2%; Pred. No. 3e-311; Matches 1998; Conservative 0; Mismatches 219; Indels 75; Gaps 14;	0y 6 ACCACCATGGGTTGGAACTGTATCATCTTTCTTGGTTACCACAGCTGTG 62	Qy 63 CACTCCCAGGTCCAGCTGGAGTCTGGGGCTGAGGTGAAGAACCTGGGAGCTCAGTG 1.22	QY 123 AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACGTGAGA 182	Oy 183 CAGGCTCCTGGACAGGGCCTCGAGTGGATTATTAATATTACTATGATAATACA 242	OY 243 AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA 302	Oy 303 GCCTATATGGAACTTAGTTCTTTGAGGATACGGCCGTTTATTACTGTGCAAGA 362	Qy 363 GCGG	OY 390 CAAGGTACCTTGTCACCGTCTCCTCAGGTGACTCTTAAAACCTCTAGAGCTTTCTGGG 449	QY 450 GCGAGCCGGACCTGACTTTGGCTTTTGGGCAGGGGGCTAAGGTGAGGCAGGTGGCG 509 1	Qy 510 CCAGCCAGGTGCACACCCAATGCCCGTGACCCCAGACACTGGACCCTGGACCCTGG 569 Db
1110 GAGGGTCTTCTGGCTTTTTCCACGGCTCCAGGCAGGCAGG	1230 AGGACCCTGCCCCTGACCTAAGCCGAAAGCCAAACTCTCCATCCTCAGCTCG 129	1518 GTCTTCCTCTCCCCCAAAACCCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1577	1578 ACGTGCGTGGTGGTGGACCACGAAGACCCCGAGGTCCAGTTCAACTGGT 1632	1633 ACGTGGACGGCGTGCATGCATAATGCCAAGACCACGGGAGGAGCAGTTCAACA 1692	1693 GCACGTTCCGTGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGG 1752	1753 AGTACAAGTGCAAGGTCTCCAACAAGGCCTCCCAGCCCCATCGAGAAACCATCTCCA 1812 	1813 AAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCAATGGACAGAGGCCGGCTCGGCCCA 1872 	1873 CCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGCCAGCCCCGAGAA 1932	1933 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCTG 1992 	1993 ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATGGCGGGGAGTGGGAGGGA	2053 CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC 2112	2113 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2172

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CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2172
 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGGAGCAGTACAACA 1725
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synthetic construct
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1 (bases 1 to 4694)
Korman,A.7., Halk,E.L. and Lonberg,N.
Human ctla-4 antibodies and their uses
Patent: WO 0114424-A 41 01-MAR-2001;
MEDAREX, INC. (US)
Location/Qualifiers
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990 CTAAGGTGAGGCAGGTGGCCCAGGTGCACCCAATGCCCGTGAGCCT 549 671 CTAAGGTGAGGCAGGTGGCCCAGGTGCACCCCAATGCCCGTGAGCCCAGACAT 126 672 CTAAGGTGACGCAGGTGGCCCAGGTGCACCCCAATGCCCGTGAGCCCAGACAT 126 673 GGACCTGGATGCACCCTGGAATAGCAAGAACCCAGGGGCCTTGGGCCCTGGGCCC 609 1127 GGACCTGTGCCACCCGGATGCAATGCCAACGGGCCTTGGGCCCTGGGCCC 186 610 AGCTTGTGCCACCCGGATCATGCGAACACCCCTCTTGAGGCCTCAAGGGCC 246 670 CATCGGTTTCCCCCTGGGCACCTGGTCCAGGACCCTCCAGAGCACCCCCTGGGCC 246 670 CATCGGTTTCCCCCTGGCCCTGGTCCAGGACCCTCCCAGAGCACCCCCTGGGCC 246 670 CATCGGTTTCCCCCTGGCCCTGGTCCAGGACCCTCCCAGAGCACCCCCTGGGGCC 246 670 CATCGGTTTCCCCCTGGCCCTGGTCCAGGACCCTCCCAGAGCACCCCCTGGGGCC 246 670 CATCGGTTCACCCTGGCCCTGGTCCAGAGCACCCCCTCGAGGCC 246 670 CATCGGTTCACCCTGGTCAATGCTCCAGGACCTCCCCAGAGCACCCCCTGGGGCC 246 671 GCTGCCTGGTCAACGATTCCCCGGAACCCTCCCCAGAGCACCCCCCTGGGGCC 246 672 GCTGCCTGGTCAACGATTCCCCCGAACCCTCCCAGAGCACCCCCCTGGGCC 246 673 GCTGCCTGGTCAACGATTCCCCCGAACCCTCCCCAGAGCACCCCCCCTGGGCC 246 674 GCTGCCTGGTCAACGATCCTCCCCGAACCCTCCCCAGAGCACCCCCCCTGGGCC 246 675 GCTGCCTGGTCAACCTTCCCCGAACCTTCCCCCAGAGCCTCAGCCCCCTGGGCCC 246 676 GCTGCCTGGTCAACCTTCCCCGAACCTTCCCTCCAGAGCTCTAACCTCACCCCCCCC	TGCCAAAAGCCATATCCGGGAGGCCTGCCCCTGCCTGCCCCAAGCCCAAAGCCAAAGCCCAAGCAAAGCCCAAAGCCCAAGCAAAGCCCAAAGCCCAAGCAAAGCCCAAAGCCCAAGCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAGCCCAAAACCCAAAAGCCCAAAAGCCCAAAAGCCCAAAAGCCCAAAAGCCCAAAAGCCCAAAACCCAAAAGCCCAAAACCCAAAAGCCCAAAAACCCAAAAACCCAAAAACCCAAAAACCCAAAAA

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1507 CAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 1566
1087 GGGGACCATCAGTTCCTGTTCCCCCCAAACCCAAGGCACCTCTCATGATCTCCCGGA 1146
CCCCTGAGGTCACGTGCGTGGTGGTGGTGTGTGTGTGTGT
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TCAACAGCACGTTCCGTGTGGGTCAGCGTCATCGTGTGTGACAGGACTGGCTGAACG 1/4
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1927 CGAGAACCACAGGTGTACACCCTGCCCCATCCCGGAGGAGATGACCAGAACCAGGTC 1986
1987 AGCCTGACCTGCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGGC 2046
2047 AATGGGCAGCCGGAGAACAACTACAAGACCACCTCCCATGCTGGACTCCGACGGCTCC 2106
2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166 1687 TTCTTCCTCTACAGCAGGCTAACCGTGGACAGGAGGAGGGGAATGTCTTC 1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] reports that the human C-gamma-4 gene is equally homologous to the mouse gamma-1, gamma-2a, and gamma-2b genes (about 75%). [3] galeo reports partial sequences for human gamma-2, gamma-3, and a gamma pseudogene. [2] presents the gamma-1, gamma-2, gamma-3, and pseudo-gamma hinge regions. This entry is part of a multigene region (region B), which includes the gamma-2, gamma-4, epsilon-1, and alpha-2 genes. See segment 1
                                                                                                                                                                                                                                                                                                        (bases 475 to 1069; 1180 to 1331; 1432 to 1655)
Takahashi,N., Ueda,S., Obata,M., Nikaido,T., Nakai,S. and Honjo,T. Structure of human immunoglobulin gamma genes: implications for evolution of a gene family
Cell 29 (2), 671-679 (1982)
                                                                            and gamma
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the gamma 2 and gamma
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Human fetal liver DNA, library of T. Maniatis [3] and Lawn et a
[1], [2]; clones 24B [1], lambda-HG4.1 [3], and Ig-gamma-4-2 [2]
Location/Qualifiers
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Ellison, J. and Hood, L.
Linkage and sequence homology of two human immunoglobu
heavy chain constant region genes
Proc. Natl. Acad. Sci. U.S.A. 79 (6), 1984-1988 (1982)
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                    2 (bases 894 to 1106)
Krawinkel, U. and Rabbitts, T.H.
Comparison of the hinge-coding segments agamma heavy chain genes and the linkage subclass genes
EMBO J. 1 (4), 403-407 (1982)
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Best Local Similarity 94.3%;
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(bassified to 4723)

Lonberg,N. and Kay,R.M.

High affinity human antibodies and human antibodies against digoxin patent: Us 6255458-A 370 03-UUL-2001;
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Korman, A.J., Halk, E.L. and Lonberg, N. Human ctla-4 antibodies and their uses Patent: WO 0114424-A 40 01-MAR-2001; MEDAREX, INC. (US)
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RESULT 14
AX088864
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KEYWORDS
SOURCE
ORGANISM

synthetic construct. synthetic construct artificial sequences. 1 (bases 1 to 4723)

REFERENCE

VERSION AX478054.1 GI:22217036 KEYWORDS SOURCE SOURCE ORGANISM STATELIC CONSTRUCT. REPERENCE 1 AUTHORS Transgenic transchromosomal rodents for making human antibodies JOURNAL Patent: WO 0243478-A 2 06-7UN-2002; Medarex, Inc. [US] ; KIRIN BERR KABUSHIKI KAISHA (JP) FEATURES I4723 SOURCE / Organism="synthetic construct" //D xref="texon:32630" Abore="features" Area Area Area Area	tch al S 1722 430 8	Db 68 CTAALGSTGAGGGGGCCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT	0y 670 CATCGGTCTTCCCCTGGCGCCTGCTCCAGAGCACCTGGGGGCCTGG 729 1	### ### ##############################	Db S43 GGAGGGTGTCTGCTGGAAGCCAGGCTCCTGCCTGCCTGGACGCATCCCGGCTATGCA 602
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Richard. Consortium/LLNL at:
High quality sequence stop: 797.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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em_estmu: *
em_estov: *
                                                                                                                                                                                                                                                                                                                                                                                                 em_estpl:*.
em_estro:*
em_htc:*
gb_estl:*
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757
990
871
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Match
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222.5
222.5
22.4
22.4
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Score

Result No.

533 530.4 506.4 505.8 504.2

Minimum DB seq Maximum DB seq

Database

Scoring table:

Perfect score:

Sequence:

OM nucleic

Run on:

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/note="Organis B-cells; Vector: pOTB7, Site 1: Xho1;
/note 2: daptor: GGCACGAG(G). Sizes=selected ->500pp
/for average insert size 1.8kb. Library constructed by Ling
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/for average in a Namer Size 1.8kb. Library constructed by Ling
/for average in a Namer Size 1.
                                                                                                                                                                                                                                                                                                      Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 974)

SS NIH-MCC Mtp://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapabs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLCM1281 row: j column: 07

High quality Sequence Stop: 801.

High quality Sequence Stop: 801.
                                                                                                                      BG398446 ... 974 bp mRNA linear EST 12-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 rcháchcergaherecradagadagacegreherrecretrececechahacechahaga 181
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                                                                                                                                                                            BG398446.1 GI:13291894
EST.
                                                                                                                                                                         mRNA sequence.
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                                                            RESULT 2
BG398446
LOCUS
DEFINITION
                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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/clone=lib="NIH_MGC_122"
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/clone=lib="NIH_MGC_122"
/clone=lib="NIH_MGC_122"
/lab hose="NIHOB"
/note="Organ: pool of 20 week female lung, 16 week female sanonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."
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23.7%; Score 533; DB 13; Length 856;
Best Local Similarity 85.8%; Pred. No. 2e-118;
Matches 646; Conservative 0; Mismatches 10; Indels 97; Gaps
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AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCATCGAGAAAACCATCTCCAAAACCAAAAGGTGGGACCGCGCGGGGTATGAGGGCCACATG 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG
                                                                                                                                                                                                                                                           CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAAGGACACCC
                                                                                                                                                                                                                                                                                                            TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC
                                                                                                                                                                                                                                                                                                                                                                                    CCGAGGTCCAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGC
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I (Dases 1 to 757)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

U Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Janes Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMOS94 row.b column: 07
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   AAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTCAGCCGTCCTCACCGTTGTG
                                   AAGCCGCGGGAGGAGCAGTACAGCACGTACCGTGTGTCAGCGTCCTCACCGTCCTG
                                                                     CACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCCAACAAAAGGCCTCCCA
                                                                                                         362 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA
                                                                                                                                                GCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCCA
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TGGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA-GCTCTGCACAAC--AT
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Location/Qualifiers
1. .757
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/db xref="rexon:9606"
/clone="IMAGE:4746150"
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/organism="Homo sapiens"
//organism="Homo sapiens"
/db.xref="Laxon:9606"
/clone=Inhealth MGC 48"
/clone=Inhealth MGC 48"
/clone=Inhealth MGC 48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="brimary B-cells, vector: porB;
/note="organ: B-cells, vector: porB;
site_2: EcoRi; cDNA made by oligo-dT priming.
Directionally cloned into EcoRifXhol sites using the Directionally cloned into EcoRifXhol sites using the following 5' adaptor: GGGAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH-MGC Library."
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I (bases 1 to 871)

S NIH-MGC http://mgc.ndi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

In Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

High quality sequence stops #488.
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602708506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 S',
mRNA sequence.
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GTGGAGTGGGAGAGCAATGGGCAGGAGAACAACTACAAGACCACACACCTCCCATGCTG
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                                                                                                                       Accaagaaccaggicagccigaccigcinginaaaggciiciaccccagcgacatcgcc
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Pred. No. 2e-111;
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EBUARYOTATE, Macroa, Chordata, Catarrhini; Hominidae; Homo.

(bases 1 to 990)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Prarayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LLCM1700 row: J column: 18

High quality sequence stop: 782.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location-Qualifiers

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1 (bases 1 to 965)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                            128 TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC
                                                                                                                                                            CTGAGGTCRAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC
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                            CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCCAAGGACACCC
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/organism="Homo sapiens"

/db_xref="taxon:9606"
/clone="InxAGE:485462"
/clone=lib="NIH MGC 48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/note="Organ: B-cells / Vector: pOTB7; Site_1: Xho1;
Site_2: BcoR1; ColNA made by oligo-dT priming.
Directionally cloned into EccRI/XhoI sites using the following S: adaptor: GGCAGGAGG; Size-selected 5500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
1 others
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Sequencing by: Tincyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov Plate: LLCMID2 row: i column: 22 Plate: LLCMID2 row: i column: 22 High quality Sequence stop: 779. Location/Qualifiers
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Pred. No. 2.1e-111;
0; Mismatches 28;
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354

294

1911

1971

437

2031

497

2091

557

2151

617

677

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Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.

En (Dases 1 to 941)

So NiH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL (Dublished (1994)

Contact: Robert Strausberg, Ph.D.

Email: capabs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

Contact: Robert Strausberg, Ph.D.

Email: capabs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

Contact: Robert Strayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLCM2474 row: C column: 04

High quality sequence stop: 638.

Location/Qualifiaers

Jurce (L. 1941)
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AGENCOURT 8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403
5', mRNA sequence.
BQ712021
                                                                                                                                                                                                       1792 CCATCGAGAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCACATG 1851
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                       295 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCCAACAACAAGAAGCCCTCCCAGCCC
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/db xref="taxon:9606"
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/ db xref="taxon:8606"
/ dlone="lmAGE:629668"
/ clone="lmAGE:629668"
/ clone="lmAGE:629668"
/ clone="lone"
/ lab host="bH10B (phage-resistant)"
/ lab host="bH10B (phage-resistant)"
/ note="organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: BCORI; DNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5. dappor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 983)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.inh.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.AG.E. Consortium (LIML)

DNA Sequencing by: Agenour Bisscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.AG.E. Consortium/LLNL at:

http://lange.llnl.gov

Plate: LLCM2469 row: k column: 12

High quality sequence stop: 604.

Location/Qualifiers

rce 1.983
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GACTCCGACGCCTCCTTCCTTCCTACAGCTCACCGTGGACAAGAGCAGGTGGCAG
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                                             511 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 570
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                                                                                                                       571 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
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22.4%; Score 504.2; DB 14; Length 983;
Best Local Similarity 83.4%; Pred. No. 2.1e-111;
Matches 628; Conservative 0; Mismatches 28; Indels 97;
                                                                                                                                                                               AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
                                                                                                                                                                                                                    631 AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 663
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AGENCOURT 8353514 NIH MGC_113 Homo
5', mRNA sequence.

BQ708975.1 GI:21847874
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ilarity 83.3%;
Conservative C
                  AĞENCOURT 7977052
5', mRNA sequence.
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/clone="IMAGE:6281403"
/clone lib="NIH MGC 113"
/lab host="NIH MGC 113"
/lab host="NIH 08 [phage-resistant)"
/note="Organ: spleen; Vector: poTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/AhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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                                                                                                                                                                                                                                                                                           81 CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCC
                                                                                                                                                                                                                                                                                                                                                      201 CTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGC
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                                                                                                                                                                                                                                              Gaps
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RESULT 9 BQ708562

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l. 873
/ organism="Homo sapiens"
/ db_xref="Laxon:9606"
/ db_xref="Laxon:9606"
/ clone="IMAGE:6215953"
/ clone=lib="NIH_MGC_113"
/ lab_bost="NHH_DB (phage-resistant)"
/ lab_bost="NHH_DB (phage-resistant)"
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/ lab_resist (phage-resistant)
/ laboratory of Gerald M. Rubin (University of California,
/ Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
/ Superscript II RT (Life Technologies). Note: this is a
// orthord
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   mRNA linear EST 16-JUL-2002 sapiens cDNA clone IMAGE:6215953
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                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Bioscience Corporation
DnA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2385 row: I column: 02
High quality sequence stop: 682.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Pred. No. 4.9e-111;
0; Mismatches 29;
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NIH_MGC_113 Homo
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BQ709771 947 bp mRNA linear EST 16-JUL-2002 EBCNCOURT 8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583 57, mRNA sequence. BQ709771
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Bukaryota, Metazoa; Chordata; Craniata; Vertebraia; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 947)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                  1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTCCCCCAAAACCCCAAGGACACCC
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                      97;
  Pred. No. 5e-111;
; Mismatches 29;
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  ilarity 83.3%; Pre
Conservative 0;
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Best Local Similarity
Matches 627; Conser
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Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metacoa; Chordata; Catarrhini; Hominidae; Homo.

1. (bases 1 to 925)
8. NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
AL Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, at:
Plate: LLCM2516 row: m column: 22
High quality sequence stop: 739.
10 catain/Qualifiers
10 catain/Qualifiers
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AGENCOURT 8485151 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6301245
5', mRNA sequence.
BQ709152
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                                               1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGAATG 1971
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                                                                                465 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG
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/organism="Homo sapiens"
/db xref="taxon:966"
/db xref="IMAGE:627599"
/clone=lib="IMAGE:627599"
/clone lib="NHH MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: poTB7; Site_1: Xho1; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into BcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                      973 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8352308 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277592
5', mRNA sequence.
BQ706204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464 row: d column: 09
High quality sequence stop: 640.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                               2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
                                                                                                          791 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACCACCACCACCACGCAG
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         GACTCCGACGCCTCCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
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NIH WGC http://mgc.nci.nih.gov/.
NITH wGC http://mgc.nci.nih.gov/.
Unbilshed (1999)
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Pred. No. 9e-111;
0; Mismatches 30; Indels
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ilarity 83.1%;
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/lab_host="DH10B" (phage-resistant)"
/note="Uorgan: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Corgan: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Corgan: spleen; Vector: pOTB7; Site_1: XhoI Site_2:
/note="Corgan: spleen; Vector of puring of construction of laborators of grand of constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CONA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
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Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I. M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LiCM2466 row: m column: 16
High quality sequence start: 3
High quality sequence stop: 675.
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Pred. No. 5.1e-111;
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/db_xref="taxon:9606"
/clone="IMAGE:6278583"
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BQ709339.1 GI:21848238
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NIH-MGC http://mgc.nci.nih.gov/.

NATH-MGC http://mgc.nci.nih.gov/.

NATH-MGC http://mgc.nci.nih.gov/.

NATH-MGC http://mgc.nci.nih.gov/.

L Dapublished (1999)

Conteat: Robert Strausberg, Ph.D.

Email: capabs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2381 row: m column: 11

*High quality sequence stop: 576.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db xref="taxon:96p6" |
/dDne="IMAGE:5450469" |
/dlone="IMAGE:5450469" |
/dlone="IMAGE:5450469" |
/dlone="IMAGE:5450469" |
/dlone="IMAGE:11" |
/lab host="HOHOB (phage-resistant)" |
/lab host="Organ: spleen; Vector: pOTB7; Site_1: Xho1; Site_2: NotE="Organ: spleen; Vector: pOTB7; Site_1: Xho1; Site_2: NotE="Organ: spleen; Vector: pOTB7; Site_1: Xho1; Site_2: NotE="Organ: spleen; Vector: pOTB7; Site_1: Xho1; Site_2: Scorii |
//dlong in the condition of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library." |
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E 1 (Bases I to 843)

E 1 (Bases I to 843)

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E 1 (Bases I to 843)

E 20 (1999)

Contact: Robert Strausberg, Ph.D.

E 20 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Ling Hong Rubin Laboratory

CDNA Library Preparation: Ling Hong Rubin Laboratory

CDNA Library Preparation: Ling Hong Rubin Laboratory

CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC column: 22

High quality sequence stop: 833.

Location/Qualifiers

1 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM007897 843 bp mRNA linear EST 30-OCT-2001
603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
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   335 CCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGG 394
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                                                                                                       395 TCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA
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Pred. No. 2.6e-110;
0; Mismatches 29; Indels 97;
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/organism="Homo sapiens"
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Best Local Similarity 83.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Context: Robert Strausberg, Ph.D.

Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM16630 row: d column: 12

High quality sequence stop: 782.

Location/Qualifiers

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                                                                                                                                                                                                                            Homo sapiens Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 797) NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCAGCACCGTCAGTCTTCCTTCCCCCCAAAACCCAAAGGACACCCTCATGATCTCCCG
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Pred. No. 1.8e-110;
0; Mismatches 18;
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                                                                                                                                  BG741164.1 GI:14051817
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ilarity 84.3%;
Conservative
                                                             mRNA sequence.
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                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
LOCUS
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ORIGIN
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AUTHORS
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JOURNAL
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Search completed: July 18, 2003, 09:26:02 Job time : 3905.3 secs

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July 18, 2003, 04:14:58; Search time 583.029 Seconds (without alignments) 8686.944 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

20	Description		pMDR1002 insert; p	DNA encoding Human	Sequence encoding	IdG1 dene. Homo s	Nucleotide semenc	Human IdGdamma4 he	Gamma heavy chain	Nucleotide sequenc	1
SUMMAKIES	ID		AAQ30910	AAS11982	AA025443	AAT60739	AAF55225	ABK85577	AAT78802	AAZ21997	
	DB	1	13	22	13	18	22	24	18	20	
	Query e Match Length DB ID									4723	
de	Query Match		80.2	78.3	77.3	77.2	72.8	72.8	71.7	71.7	
	Score		1804	1761.2	1739.4	1736.2	1638	. 1638	1611.8	1611.8	
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ABK85576 AA039243 AA039099 AA0250099 AA0250099 AA779856 AAA76891 AAA76891 AAA6891	AAQ33846 AAT77388 AAT77388 AAA77080 AAA7184 AAA11622 ABL46001 ABL48744 AAV70079 AAA72159 AAA11597 ABL45976 ABL46719
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ALIGNMENTS

AAQ30910 standard; DNA; 2560 BP.

RESULT 1 AAQ30910

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Vector; pWDR1002; NotI; HindIII; pWDR1001; pSAB132; pBAG101; E. coli; JA221(Iq); ampicillin; resistance; immunoglobulin; signal sequence; humanised; SAB; heavy chain; variable; region; HV; 1gG4; constant; HC; antibody; homolog; CD4; gp120; cell surface glycoprotein; CD4+; lymphocytes; helper; inducer; HIV; syncytia; formation; ss.
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/*tag= b
//tote= "Immunoglobulin signal sequence"
69..2296
/*tag= c
                                         pMDR1002 insert; pre-5A8 humanised heavy chain.
                                                                                                                                                Location/Qualifiers
12..2299
                     (first entry)
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/*tag= d
/number= 1
436..711
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                                                                                                                                                                                                                                                                                           /number=
                                                                                                                              Homo sapiens
                     02-APR-1993
                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                  mat_peptide
AAQ30910;
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1030 GCCCCAGCCCAGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
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                                                           CCAGGTCCAGCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT 127
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GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCCTGGGCCC 609
                                                                                         68 ccaggrccaacrgcaggagrcrggagcrgaagrgaaaagccrggggcrrcagrgaaggr
                                                                                                                                                                                  188 TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the insert of the vector pWDR1002. Three fragments were used in the construction of pWDR1002, a 443 bp Not! I fragment were used in the construction of pWDR1002, a 443 bp Not! I HindIII fragment of pWDR1001 (see AAQ30905), the 7913 bp Not! I linearised pSAB122 (see AAQ30909). These fragments were ligated together and the ligation mixture was used to transform E. coli JA221(Iq) to ampicillin resistance. The insert encodes the immunoglobulin signal sequence, amino acids (AA) 1-122 of the humanised SAB heavy chain, is: the constant region (HV) and AA114-AA478 of the human 1gG4 heavy chain, is: the constant region (HC). The polypeptide encoded by this sequence is an antibody homolog which was shown to bind to CD4 but did not block the binding of gpl20 to CD4. CD4 is a cell surface glycoprotein of induced syncytia formation. This homolog can be used in the induced syncytia formation. This homolog can be used in the detection, prophylaxis and treatment of diseases caused by infective constant whose primary targets are CD4+ cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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larity 89.2%; Pred. No. 0;
Conservative 0; Mismatches 185; Indels 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New anti-CD4 antibody homolognes - which bind CD4, do not b
binding of HIV gpl20 to CD4 but block HIV-induced syncytia
formation between CD4+ cells
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/ number= 4
/ note= "Human genomic IgG4 HC"
/ tag= k
/ number= 4
1977. 226
/ number= 1
/ number= "Human genomic IgG4 HC" -
/ stag= "AA1-AA122 of humanised 5A8 VH'
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*tag= h

/note= "Human genomic IgG4 HC"

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*tag= i

/number= 3

1550.1879
712..1005
*tag= f
/number= 2
/note= "Human genomic IgG4 HC"
1006..1395
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/number= 2
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P-PSDB; AAR28808.
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Matches 2049; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-1991;
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2165 TTCTTCCTCTACAGCAGCTAACCGTGGACAAGAGCAGGAGGGAG	RESULT 2 AAS11982 ID AAS11982 X X X AC AAS11982; XX XX XX AC DT 04-DEC-2001 (first entry) DT 04-DEC-2001 (Husanised monoclonal antibody Hu266, heavy chain.	Monoclonal antibody; Hu266 Alzheimer's disease; Down'heavy chain; ds; gene ther Mus sp. Homo sapiens. Synthetic. Key CDS 12235 CDS 7*tag= a	sig_peptide 12.68 /tag= b /tag= b /stag= b /stag= b /stag= c /stag= c /stag= c /stag= c /stag= c /stag= d /number= l /number= l /number= l /number= l /number= c /stag= c /sta	0 10 10 14 18	intron / rag= 1 / rumbe= 4 / numbe= 4 / stag= 1 / rag= k / rag= k / number= 4 / 1913. 2235 / rag= 1 / number= 5 / rag= 1 / number= 5 / rag= 1 / number= 5 / rag= 1 / number= 5 / rag= 1 / number= 5 / rag= 1 / number= 5 / rag= 1 / number= 5 / rag= 1 / number= 5 / rag= 1 / rag
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	1210 TGCCBAAAGCCATATCCGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA	1385 TCTCTCTGCAGATCCAAATATGGTCCCCCATCATGCCCAGTAGCTAAGCCCAACCCA 1444 1390 GGCCTCGCCCTCAAGGGGGACAGGTCCCCTAGAGTAGCTGGATCCAGGGACA 1449	1565 GGGGALCATCHICLTCCTGTTCCCCCAAACCCAAGGACACTCTCATGATCTCCCGGA 1624 1567 CCCCTGAGGTCACGTGGGGGGGGGCGTGCACGCACGAGGACCCTCTCATGATCTCCCGGA 1624 1628 CCCCTGAGGTCACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTCCAGGTTCA 1684 1627 ACTGGTACGTGGTGGTGGTGGTGGTGGAGGTGCAAGACCCGGGGGGGG	TCTCCAAAGCCACTGTGGGGCGGGGGTATGGGGCCCCATGGGACTGGCTGACGGGCGACGGGGCTGACGGGCTGACGGGCTGACGGTGTGGTCAGGGCTCTGCACCGTCCTGCACCGGCCCCATGGGCTGACGACGGCGCGACGGGGCTGGCT	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      The IgG1, in its nascent form, bears no sialy1-Lex side chains. The inventors designed a molecule including several such sites for attachment of sialy1-Lex side chains (see AAR2442, FT). The additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding ability. They are preferably located in the CH2 region of the Ig molecule. Antibodies bearing multiple sialy1-Lex determinants are useful for disrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92;
                                                                                                                                                                                                                                                                                              Inhibition of cell adhesion mediated through ELAM-1 mol. bind:
- used in treating chronic inflammation, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 1, 46pp; English.
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                                                                                90US-0618314.
                                   91WO-US08605
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Matches 2036; Conservative
                                                                                                                             (GEHO ) GEN HOSPITAL
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P-PSDB; AAR24442.
                                                                                                                                                                             Walz G;
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                                   18-NOV-1991;
                                                                              23-NOV-1990;
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                                                                                                                                                                                         The gene (AAT60739) encoding 1gG1 (AAW10550) can be subjected to sitedirected mutagenesis in order to introduce one or more N-linked glycan addition sites into the 1gG1 molecule (see also AAW10551). Bukaryotic host cells co-transfected with a vector carrying the the mutated 1gG1 gene and with a vector that expresses an alphatia Stucosyltransferase capable of attaching sialy1-Le(x) groups at the glycosylation sites of the antibody molecule can be used in the prodn. of sialy1-Le(x)-modified antibody. Such an antibody has therapeutic applns. e.g. in minimising inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTCCCAGGTGCAGCTGCTGCAGTCTGGGGCTGAGGTGAAGAAGAAGCCTGGGTCCTCGGTG
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                                                                                                                                                                                                                                                                                                                                    decreasing extravasation-dependent organ damage and/or clotting
                                                                                                         mol. - having
for protecting
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 188; Indels
                                                                                                                                                                                                                                                                                                                                                                Sequence 2287 BP; 483 A; 758 C; 648 G; 398 T; 0 other;
                                                                                                      P-selectin and opt. E-selectin binding organic sialyl-Le(x) and sulphated determinant, useful against inflammatory or immune reactions
                                                                                                                                                                  Disclosure; Page 40-41; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9%;
Matches 2034; Conservative
 CORP.
GEN HOSPITAL
                                                          WPI; 1997-077356/07.
P-PSDB; AAW10550.
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Sat Jul 19 10:01:49 2003

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us-09-627-896b-23.rng	XX PT NOVE P.		XX Example 10; Page 94-95; 127pp; English. CC The present sequence is the pres	C human -vacuon describes used in the course of the specification. The C antibodies are used hyphocyte associated which specification. The CC antimule response in methods fociated antique, specifically binding CC his methods for a second antique.	CC also useful for treating antigen in a patient, where the prolonging CC exacerbated by increased activity of insands. The antibodies CC antie, melanoma or cativity of disease in a shift antibodies.	or microody prepries of epithelias of Cells of Subject canada are
1698 TTCCGTGTGGTCAGGGTCGTTCACGGTTCACAGGTTCAGGTTCAGGTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTC	1751 TACCGGGTGGTCCTCACCGTCCTGCAGGGGTGGCTGAACGGCAAGGAGTAC 1757 1758 AAGTGCAAGGTCCTCACCGTCCTGCACCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGAGGGGTGGT	1818 AAAGGTGGGACCCGCGGGCCTCCCAGCCCCATCGAGAAACCATTCCAAAACC 1817 1851 AAAGGTGGGACCCGCGGGGGTATGAGGGCCAAATGAGAGAAAACCATCTCCAAAGCC 1850	1878 TGCCCTGGGAGTGACCGCTGTGGCGAGGCCACTGGTGGACAGAGGCCGGCC	1938 GOTGTACACCTGCCCCATCTACCAÁCCTTGTG-CTAGAGGGAGCCCCCAAGAGGGAGCCACCAA 1937 1970 GGTGTACACCTGCCCCCCCCCCGGAGAGAGAGAGAGGCAGCCCCGAGAACCACA 1969	1998 CCTGGTCAAAGCTTCTACCCCATCAGGTGACTCACCAAGAACCAGGTCAGCTGACCTG 1997 2030 CCTGGTCAAAGCTTCTACCCCAGCGATGACTCACCAAGAACCAGGTCAGCTCACTG 2029	COLUMN TO THE CO

The present sequence is used in the course of the specification. The present sequence is used in the course of the specification. The fundant of the specification describes a human antibodies which specification. The cantibodies are used in methods for inducing, augmenting or produce to an antigated antigan-4 (CTLA-4). Such that is useful for treating autoinmune disease the willowing the antibodies of cancer, melanoma or epithelial cancer. The antibodies are cantibody proparation comprising two antibodies of the inducing prostate of the suppressing a immune response in a subject caused or treating cancer, infectious diseases and promoting prostate cancing cancer, infectious diseases and promoting beneficial autoinmune for suppressing a immune response in a parient. They are used for reacting cancer, infectious diseases and promoting beneficial autoinmune of diseases with inflammatory or allergic cancer; and inflammatory or allergic contains and lupus erythematosus, multiple clerosis, insulin-dependent contains are used for disease. The contains a the invention and inflammation, graft versus \$

Sequence 4694 BP; 1068 A; 1396 C; 1248 G; 982 T; 0 other; à

Ouery Match Best Local Similarity 72.8%; Score 1638; DB 22; Length 4694; Matches 1719; Conservative 0; Mismatches 95; Indels 4;

490 CTAAGGTGAGGCAGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGGCCCAGACACT 549 67 Craddotancocaegiodocaeccaegocaeccaeacccaatoccaranoccaeacaeccaearaeacccaacaecaeacae 126 550 GGACCCTGCTGGACCTGGGATAGACAAGAACGGAGGGCCTCTGGGCCCTGGGGCCC ò Ω à

610 AGCTCTGTCCCAACACCGCGGTCACATGGCACCACCTCTTGCAGCCTCCACCAAGGGCC 669 Db ò СP ò ОP

730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGGTGGAACTCAGGGCCTC 789 ò

790 TGACCAGCGGCGTGCACCTTCCCAGCTGTCCTACAGTCCTCAGGGACTCTACTCCCTCA 849 дq

Complementarity determining region, CDR, immune response; antibody, cytcoxic Tymphocyte associated antigen-4. CTLA-4, B7 lishody, the associated antigen-4. CTLA-4, B7 lishody, the multiple scletosis, infectious disease; inf. CTLA-4, B7 lishody, multiple scletosis; insultand gravis, lupus exythematosus, transplant rejection, graft dependent diabetes mellitus, exythematosus, constitution, graft Versus host disease, ss.

RESULT 5

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5225 AAF55225 standard; DNA, 4694 BP.

2270 ATGAGTG 2276

Nucleotide sequence of pG4HE. 29-MAY-2001 (first entry)

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24-AUG-2000; 2000WO-US23356,

01-MAR-2001.

24-AUG-1999,

99US-0150452

Korman AJ, Halk EL, (MEDA-) MEDAREX INC.

WPI; 2001-202933/20.

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850 GCAGCGTGGGTGCGCTCCAGCAACTTTGGGCACCCAGACCTACACCTGCAACGTAG 909

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel transgenic nonhuman mammals, particularly rodents, comprising two human immunoglobulin (Ig) loci, where one of two the human immunoglobulin loci is a human heavy chain locus and the other locus is a human light chain locus, and where only one of the loci is of a transchromosome. The transgenic animals are useful for generating a number of B-cell expressing human artibody sequences. They are also useful for producing rearranged immunoglobulin sequences, producing human antibody display libraries, and generating a human sequence antibody that binds to a predetermined antigen. The produced antibodies are useful for treating immune-related disorders. The present sequence represents a plasmid used in the construction of expression vectors for human IgG.
TICTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTC
                                                                    TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 AACCICIAGAGCITICIGGGGCGAGCCGGGCCTGACITIGGCTTTGGGGCCAGGGAGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New transgenic nonhuman mammal, useful for generating B-cells expressing human antibody sequences and generating antigen-specific hybridomas secreting human sequence antibody, comprises two human
                                                                                                                                                                                                                                                                                                                                                                B-cell;
mutant;
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human antibody display library; immune-related disorder;
immunomodulatory; IgGgamma4 heavy chain; pG4HE; cyclic;
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                                                                                                                                                  A novel composition has been developed which comprises an immunoglobulin (1g) having an affinity constant (Ka) of at least 2 multiply 100000000 M-1 for binding to a predetermined human antigen. The present 100000000 M-1 for binding to a predetermined human antigen. The present sequence represents the kappa light chain plasmid pCKY-96 which includes the human gammal constant region and polyademylation site. Anti-CD4 antibodies may be used in therapeutic and diagnostic applications especially for the treatment of human diseases. These antibodies reduce activity of CD4 cells and reduce undesirable autimmune reactions, inflammatory response and transplant rejection. Transplant significant are capable of producing heterologous antibodies of multiple isotypes by undergoing isotype switching. These animals produce a first ig type that is necessary for antigen-stimulated B-cell maturation and can serious antipolate and recode and produce one or more subsequent heterologous
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71.7%; Score 1611.8; DB 18; Length 4723;
Best Local Similarity 94.3%; Pred. No. 1.7e-313; Indels 18; Katches 1722; Conservative 0; Mismatches 87; Indels 18; K
                                                                                                                                                                                                                                                                                                                                        Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;
                                                                                                                                Example 42; Page 262-264; 396pp; English.
                                                                                           Novel anti-CD4 antibody produced by tr
treatment of auto-immune disease etc.
10-OCT-1995; 95US-0544404.
                        (GENP-) GENPHARM INT INC.
                                                                      WPI; 1997-235888/21.
                                              Lonberg N;
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Lonberg

Halk EL,

2001-202933/20

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The present sequence is used in the course of the specification. The specification describes a human antibodies which specifically bind to human cytocoxic T lymphocyte associated antigen-4 (CTLM-4). Such antibodies are used in methods for inducing, augmenting or prolonging an immune response to an antigen in a patient, where the antibodies are block binding of human CTLM-4 to human B7 ligands. The antibodies are also useful for treating autoimmune disease in a subject caused or exacerbated by increased activity of T cells and for treating prostate cancer, melanoma or epithelial cancer. A polyvalent or polyclonal antibody preparation comprising two antibodies of the invention are useful for suppressing a immune response in a patient. They are used for treating cancer, infectious diseases and promoting beneficial autoimmune reactions for the treatment of diseases with inflammatory or allergic components. The polyvalent or polyclonal preparations are useful for treating autoimmune diseases such as rheumatoid arthritis, myasthenia gravis and lupus erythematosus, multiple sclerosis, insulin-dependent contents.
                                                                                                                                                                                                                                           Novel human sequence antibody that binds to human cytotoxic T lymphocyte associated antigen-4, useful for inducing, augmenting prolonging immune response to antigen or for suppressing immune
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24-AUG-2000; 2000WO-US23356
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response in patient
                                                                                        (MEDA-) MEDAREX INC
                                                                                                                                  Korman AJ,
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AAF55224 standard; DNA; 4723

(first entry)

29-MAY-2001

AAF55224;

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                       G; 987 T; 0 other;
                                           Score 1611.8; DB 24; Lengt
Pred. No. 1.7e-313;
0; Mismatches 87; Indels
 for human 1gG
                      Sequence 4723 BP; 1072 A; 1411 C; 1253
   expression vectors
                                           Query Match
Best Local Similarity 94.3%;
Matches 1722; Conservative
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Transgenic animal; human heterologous antibody; transgene; isotype switching; neutrophil efflux; reperfusion injury; CD4 binding; autoimmune reaction; inflammatory response; transplant rejection;

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The plasmid is used in the construction of minigenes for expression of 100 plasmid anti-CD4 antibodies, in the transgenic mouse of the invention. The plasmid anti-CD4 antibodies, in the transgenic mouse of the invention.

The specification describes transgenic non-human animals, especially a mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenic animals have human heavy and light chain transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (ig) light chain transgene comprises at least one V and J gene segment, region gene segment. The immunoglobulin (ig) light chain transgene comprises at least one V and J gene segment.

The antibody can be used to prevent efflux of neutrophils from the sequents are labored to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to read to rea
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acid induced lung injury; acute adult respiratory distress syndrome;
ARDS; vasculitis; septic shock; allergic reaction; asthma;
cystic fibrosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.6%; Score 1610.2; DB 19; Length 4723; Best Local Similarity 94.2%; Pred. No. 3.6e-313; Matches 1721; Conservative 0; Mismatches 88; Indels 18; G
                                                                                                                                                                                                                                                                                                                                                                                                 Hybridoma producing antibody specific for interleukin-8 - used prevent efflux of neutrophils from vasculature, and treat reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4723 BP; 1072 A; 1410 C; 1253 G; 988 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 42; Pages 312-315; 452pp; English.
                                                                                                                                                                                                           97WO-US21803.
                                                                                                                                                                                                                                               96US-0758417.
                                                                                                                                                                                                                                                                                    (GENP-) GENPHARM INT.
                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-333306/29.
                                                                                                                                                                                                                                                                                                                         Kay RM, Lonberg N;
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pBAG101 was designed to carry genomic DNA encoding the human IgG4 heavy chain constant region. The IgG4 DNA was isolated by polymerase chain reaction from human placental DNA using the primer sequences given in AA303097-08. The amplification product of this reaction was approx. 2109 bp. This fragment was inserted into EcoRS linearised pNN03 (see also AAQ3056) to give the intermediate plasmid pBAG101.
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                                                                                                                   DB 13; Length 2029
                                                                                                                71.6%; Score 1609.2; DB 13; Lengt
94.5%; Pred. No. 5.1e-313; .
.ive 0; Mismatches 93; Indels
                                                                                        Sequence 2029 BP; 423 A; 710 C; 564 G; 331 T; 1 other;
                                                                                                                                             Matches 1711; Conservative
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Oy 1338 CAGAGGGGAAATGTTGTGTTGTTGTTGTTGTTGTTGTTGTT	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Db		Cy Db Db Db Db Db Db Db Db Db Db Db Db Db	AC AC AC AC AC AC AC AC AC AC

Qy 1747 GCAAGGATACAAGTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAACCA 1806 Db 1316 GCAAGGATACAAGGTCTCCAACAAAGCCTCCCAGCCCCCATCGAGAAAACCA 1375 Qy 1807 TCTCCAAAACCAAAGGTGGGACCGGGGGTATGAGGGCCACATGGACAGAGGCGGGTT 1866 Db 1376 TCTCCAAAACCAAAGGTGGGACCGGGGGTATGAGGGCCACATGGACAGAGGCGGGTC 1866 Db 1376 TCTCCAAAGGTGGGACCGGGGGTACGGGGCACATGGACAGAGGCGGCTC 1435 Qy 1867 GGCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACGTGCCCTACAGGGCAGCCC 1435 Db 1436 GGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACGGCAGGCCC 1495 Qy 1927 CGAGAACCACAGGTACAACCTGCCCCATCCCGGGAGGAGAGACAACCAAGAACCAAGAACCAACAACCAACAA	1997 AGCCTGACCTGGTCAAAGGCTTCTACCCCAGCGACATGACCAAAACCAAGGTC 204 1987 AGCCTGACCTGGTCAAAGGCTTCTACCCCAGCGACTGGCGTGAGTGGGAGAGC 204 1556 AGCTGACCTGGTCAAAGGCTTCTACCCCAGCGACTGGTGGAGTGGGAGAGC 204 1556 AGCTGACCTGGTCAAAGGCTTCTATCCCAGCGATCGGTGGAGTGGGAGAGC 204 1616 AATGGGCAGCCGGAGAACAACTACAAGACCAACCTCCCATGCTGGACTCCGACGGCT 161 1616 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC 210 1616 AATGGGCAGCCGAGAACAACTACAAGACCAACGCCCTCCCGTGCTGGACTCCCACGGCTCC 167 2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGCGGGAACGTCTTC 216 1676 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGCAGGAGAACGTCTTC 173 2167 TCTTCCTCTACAGCAAGCTCACCGTGGACAACACACTACACGCAGAAGAGCCTCTCCCTG 222 1161	Oy 2227 TCCCGGGTAAATGAGTG 2244	Encodes CD4-IgG homodimer; solu chimeric; incre Homo sapiens ch Key CDS	FT CDS 1374.1408 FT (Abel= hinge domain 1744.1408 FT (Abel= hinge domain 1758.1854 FT (Abel= CH2 domain 176.2275 FT (Abel= CH3 domain 176.2275 FT (Abe
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                   GA, Maddon PJ;
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This sequence encodes a CD4-gamma2 chimeric heavy chain homodimer.

0.7 kb fragment, and cloned into M13mp18 forming M13mp18 (CD4). This was linearised with Pst1, and the SacII(flush) Pst1 fragment from Dbr gamma2 containing human gamma2 heavy chain (CH1 excn) isolated and ligated to the M13mp18 (CD4) vector. Resulting recombinants were then Streened by restriction analysis for the presence of both CD4 and CH1 which occur in trandem CD4 (BcoR1/Stu1) -CH1 (SacII(flush)/Pst1). CH1 which occur in trandem CD4 (BcoR1/Stu1) -CH1 (SacII(flush)/Pst1). CH1 which occur in trandem CD4 (BcoR1/Stu1) -CH1 (SacII(flush)/Pst1). CH1 heavy chain sequences in frame. The resulting chimeric DNA molecule encodes a protein containing the V1V2 domains of CD4 fused with the correct sequence were then grown in Td1 cells and Rf DNA isolated from the cells. CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for treatment; prevention and diagnosis of HIV infection Claim 13; Fig 4; 90pp; English.

Sequence 2482 BP; 559 A; 812 C; 676 G; 435 T; 0 other;

ò 714 AGCACAGCGGCCCTGGGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773 1013 1047 CCGGAGGCTCTGCCCGCCCCATGCTCAGGAGAGAGGTCTTCTGGCTTTTTCCACC 1133 TACACCTGCAACGTAGATCACAAGCCCAAGCAACACCAAGGTGGACAAGACAAGTTGGTGAG 953 0; Gaps AGGCCAGCTCAGGGAAGGGAGGGTGTCTGCTGGAAGCCAAGGTTCAGCCCTCCTGCTGGAC Ouery Match
Best Local Similarity 99.7%; Score 1584.6; DB 13; Length 2482;
Matches 1587; Conservative 0; Mismatches 4; Indels 0; C

1287 1313 1347 1434 CCTGCATCCAGGACAGGCCCCAGCTGGTGCTGACACGTCCACCTCCATCTTCCTCA 1493
1468 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTTCCTCA 1527 1408 CAGGTAAGCCAGGCCTCGCCTCCAGGTCAAGGCGGGACAGGTGCCCTAGAGTAG 1467 GCACCAACTGCGGGAGCAGCGGTGTTCCTCTTCCCCCAAAAGCGCAAAGGACGCTC 1553 1528 GCACCACTGTGGCAGGACGGTCAGTTTCCTCTTCCCCCCAAAACCCAAGGACACTT 1587 1554 ATGATCTCCCGGAACCCCTGAGGTCACGTGGTGGTGGTGGAGGTGAGCGTGAGGAGAGGCCT 1613 1647 1614 GAGGICCAGIICAACIGGIACGIGGGGIGGAGAGAGAAAATGCCAAGACAAAGCCA 1673 1767 1827 1828 ATCGAGAAAACCCAAAACCAAAGGTGGGACCGGGGGGTATGAGGGCGACATGGA 1887 1794 ATCGAGAAAACCATCTCCAAAAACCAAAAGGTGGGACCCGGCGGGGGTATGAGGGCCACATGGA 1853 1913 2007 2067 1947 2033 2093 CTCCGACGGCTCCTTCTCTCTTACAGCAAGCTCACGGTGGACAAGAGCAGGTGGCAGCA 2128 CTCCGACGGCTCCTTCCTCTACAGCAAGCTCACCGTGGACAAAGCAGGTGGAAGA 2187 2247 GIGCTTGGCTCAGACCTGCCAAAAGCCCATATCCGGGAGGACCCTGGCCCCTGACCTAAAGCC 1588 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGACGTGAGCCACGGAGACCCC والإطاعة والمعادة وا 1948 TACAGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGAC <u>caadaaccaggricaggcrigaccriggricaaaggcrircraggggricagggacarcgg</u> 2034 GGAGTGGGAGAGAATGGGCAAGCGGAAGAACTACAAGACCACACACCTCCCATGCTGGA GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAACGCAGAA GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2278 1228 1494 1734 1768 1888 1854 1974 2094 2248 (2154 d V ò 면 당 연 임 ò qq ò Op ò Dp ò 90 A0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the CD4-IgG2 chimeric heavy chain nucleotide sequence from the CD4-IgG2 chimeric heterocetramer. The invention relates to an immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer of two heavy chains and two light chains. The cytotoxic radionuclide is linked to either the heavy chains or the light chains, or chains are chimeric CD4-IgGalfc-pacCWV (ATC7 CF191) and both light chains are chimeric CD4-kappa chains are chimeric CD4-KDC-pRCCWV (ATC7 75194). CD4 is a con-polymorphic cell surface glycoprotein that is expressed on the surface of helper T lymphocytes, cells of the monocyte/macrophage lineage and dendritic cells. CD4 sociates with major histocompatibility complex and dendritic cells. CD4 surface of antigen presenting cells to mediate efficient cellular immune response interactions. In humans CD4 is the target of interaction with the human immunodeficiency virus HIV. The immunoconjugate is used to kill cells infected with HIV, and for treating construction in the immunoconjugate is used to kill cells infected with HIV, and for treating construction in the immunoconjugate is used to diffection, and for assessing efficiency of treatments). The immunoconjugate is the target of determined the HIV construction is used to interaction, and for assessing efficiency of treatments). The immunoconjugate is also used to determine the HIV construction is used to interaction is used to interaction is used to interaction is used to interaction is used to interaction is used to interaction is used to interaction is used to interaction is used to interaction is used in the interaction is used to interaction is used to interaction is used to interaction is used to interaction is used to interaction is used to interaction is used in the interaction is used to interaction is used to interaction is used to interaction is used in the interaction is used in the interaction is used in the interaction is used in the interaction is used in the interaction is used in the interaction is used
                                                                                                                                                                                                                  CD4-IgG2 chimeric heavy chain heterotetramer; immunoconjugate; treatment; cytocoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging; prognosis; ervelope glycoprotein burden; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD4 spling interaction is essential for infection). The heterotetramers are assembled intracellularly and secreted efficiently from mammalian cells, allowing high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunoconjugate, used to treat, prevent or image human immune deficiency virus infection, comprises radionuclide attached to heterotetramer of CD4-immunoglobulin chimeras
                                                                                                                                                                              CD4-1gG2 chimeric heterotetramer heavy chain nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the staging and prognosis of HIV infected patients. The immunoconjugate should be active against all strains of HIV
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                                                       AAZ98856 standard; cDNA; 2482 BP
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95US-0379516.
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TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
TITLE OF INVENTION: GRERTRUIDA M.
TITLE OF INVENTION: GRERTRUIDA M.
TITLE OF INVENTION: GRERTRUIDA M.
TITLE OF SOURVENT SOURS.
CURRENT REPERENCE: 09702.0081.00000
CURRENT RILNG DATE: 1999-02-12
SOFTWARE: PARCHIN VOR: 2.1
SOFTWARE: PARCHIN VOR: 2.1

Sequence 23, Application US/09249011A Patent No. US20020176855A1

US-09-249-011A-23

Sequence 5', Applisequence 2', Applisequence 3', Applisequence 2', Applisequence 2', Applisequence 5', Applisequence 16', Applisequence 116', Applisequence 116', Applisequence 142', Applisequence 144', Applisequence 156', Appl Sequence 23, Appl Sequence 55, Appl Sequence 3, Appli Sequence 57, Appli Description 1 US-09-249-011A-23 5 US-10-047-542-55 5 US-10-00433-3 5 US-10-000-433-2 US-08-485-163-4 0 US-08-485-163-4 0 US-09-163-382-2 5 US-10-07-075-29 5 US-10-16-484-116 5 US-10-216-484-184 5 US-10-216-484-144 5 US-10-216-484-146 5 US-10-216-484-146 5 US-10-216-484-154 5 US-10-216-484-154 5 US-10-216-484-154 5 US-10-216-484-154 5 US-10-216-484-154 5 US-10-216-484-154 SUMMARIES Query Match Length DB 100.0 79.5 72.8 71.7 71.7 70.5 70.5 70.3 68.8 68.8 2249 1787.6 16138 16138 16138 15884.6 15884.6 15884.6 15884.6 1588.6 1455.4 1455.4 1455.4 1455.4 Score Result Š.

FEATURE: NAME/KEY: CDS LOCATION: (1341)..(1376) FEATURE:

NAME/KEY: CDS LOCATION: (655)..(948)

FEATURE

FEATURE: NAME/KEY: CDS LOCATION: (12)..(417) ORGANISM: Mus sp.

TYPE: DNA

LENGTH:

NAME/KEY: CDS LOCATION: (1495)..(1821)

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                                          Query Match

100.0%; Score 2249;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2249; Conservative 0; Mismatches
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2041 GAGAGCAATGGGCAGCGGAGAACAACTACAAGACCACCTCCCATGCTGGACTCCGAC 2100	2101 GGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGGGAAC 2160 	2161 GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC 2220	2221 TCCCTGTCCCGGGTAAATGAGTGAATTC 2249 	SULT 2 -10-047-542-55	Sequence 55, Application US/10047542 Publication No. US20020168367A1 GENERAL INFORMATION: APPLICANT: LARRICK, JAMES W.	FFILCHNII WICOFF, MALIN D. ITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL ITLE OF INVENTION: AND BACTERIAL DISEASES ILE REFERENCE: 030905.0004.CIP1	URRENT FILIUS DATE: 2001-10-26 TRIOR APPLICATION NUMBER: PCT/US01/13932 RIOR FILING DATE: 2001-04-28	PRIOR APPLICATION NUMBER: 60/200,298 PRIOR FILING DATE: 2000-04-28 NUMBER OF SEQ ID NOS: 101 SOFTWARE: Patentin Ver. 2.1	LENGTH: 2009 TYPE: DNA ORGANISM: Homo sapiens	79.5%; Score 1787.6; DB 15; Length 2009; 99.7%; Pred. No. 0;	seccasece		51 GGLAGGIGGCCCCAGGIGGACACCCAGIGAGCCCAGACACTGGACCCTGC 120 559 CTGGACCCTCGTGGATAGACAAGAACCGAGGCCCTTGGGCCCTGGGCCCAGCTCTGTC 618 13. TTGGACCTTGTAATAAAAACCAAGGACCTTTTGCCTTTGTC 17.0	CCACACCGCGGTCACATGGCACCTCTTTGCAGCCTCTGGGCCCAGGCCCAGGTCTGTC CCACACCGCGGTCACATGGCACCTCTTTGCAGCCTCCACCAAGGGCCCATCGGTCT	TCCCCCTGGCCCTGCTCCAGGACCTCCAGAGACCTCCAGGAGCCCTGGTTCCAGGAGCCCTGGGGCTTCCAAGAGCACCTCCGAAGAGCACCTCCGAAGAGCACCTCCGAAGACACCTCCGAAGACACCTCCGAAGAGCACCTCCGAAGAGCACCTCCGAAGAGCACCTCCGAAGAGCACCTCCGAAGAGCACCTCCGAAGAGCACCTCCGAAGAGCACCTCCGAAGAGCACCTCCGAAGAGCACCTCCAAGAACACCTCCAAGAAGAACACAACAACAACAACAACAACAACAACAAC	739 TCAAGGACTACTTCCCGGAACCGGTGACGTGTGGAACTCAGGGGCTCTGACCAGG 798	8 4 0

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Qy 619 CCACACGGGGTCACATGGCACCTCTTTTGCAGCTCCACCAAGGGCCCATGGGTTCACAAGGGCCCATGGTTCACAAGGGCCCATCCGTTCACAAGGGCCCATCCGTTCACAAGGGCCCATCCGTTTTTGCAGCACTCTCACCACAAGGGCCCATCCGTCTTTTTTTT	Qy 679 TCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACACAGGGCCCTGGGCTGCCTGG Db 240 TCCCCCTGGCGCCTGCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCTGGGCTGCCTGG	739 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCT	GCGTGCACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCT	Qy 859 IGACCGIGCCCTCCAGCAACTITCGGCACCCAGCCTACACCTAGATCACAAGC	Qy 919 CCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGG	Oy 979 CTGCTGGAAGCCAGGCTCAGCCCTCCTGCAGACCACCCCGGCTGTGCAGCCCCAGCC	0y 1039 CAGGGCAGCAAGGCCCCCATCTGTCTCCTCACCCGGAGGCTTTGCCCGCCC	Qy 1099 ATGCTCAGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCAGGCAGG	Qy 1159 TGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACTGCCAAAAG Db 719 TGCCCCTACCCCAGGCCCTGCGCATACA-GGGCAGGTGCTGCGCTCAGACCTGCCAAAGAG	Oy 1219 CCATATCCGGGAGCACCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACT	Qy 1279 CCCTCAGCTCGGACACCTTCTCCTCCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGC	OY 1339 AGAGCGAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGGCCTCGCC	0y 1399 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGC	Oy 1459 IGGGTGCTGACGTCCACCTCTTCCTCAGCACCACTGCGGCAGCACCGT	Oy 1516 CAGICITCCICICAAAACCCAAAGGACACCTCAIGAICTCCCGGACCCCTGAGG	CTGGTA CTGGTA CAACAG	119
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US-10-000-433-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87; Indels
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71.7%; Score 1611.8;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 1722; Conservative 0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,163
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
RECISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II;1-PCT-US
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1584.6;
Pred. No. 0;
0; Mismatches
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99.7%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 2482 base pairs
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Matches 1587; Conservative
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                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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US-08-485-163-4
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 1082 AACTCCTGGGGGGGCCGTCGGTCTTCCTCTTCCCCCAAAACCCAAAGGACACCCTCATGA
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; Publication No. US20020098191A1
; GENERAL INFORMATION:
   APPLICANT: Beaudry, Gary A.
   APPLICANT: Maddon, Paul J.
   TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
   NUMBER OF SEQUENCES: 10
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Cooper & Dunham LLP
   STREET: 1185 Avenue of the Americas
   CITY: New York
   STATE: New York
   STATE: New York
   STATE: 10036
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
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us-09-627-896b	Sat Jul 19 10:01:52 2003	Db 1588 ATGATCTCCCGAACCTCGACGTCGCTGGTGGTGGTCGACGACGACGAAGCCC 1613 Oy 1588 ATGATCTCCCGGACCCTGAGTCACGTGCTGGTGGTGACGTGAGCCACGAAGACCT 1613 Db 1588 ATGATCTCCCGAACCTCGACGTCGTCGTGGTGGTGATATGCCAAGACAAACCA 1707		DD 1734 GACTGGCTGAACGCAAGGAGTHCLAAGTGCAAGGAGGCCTCCCACGCAGGAGGCCTCCCACGCAGGAGGCCTCCCACGCAGGAGTGCAAGGAGTGCAAGGAGTGCAAGGAGTGCAAGGAGTATGAGGAGCCGGGGGGTATGAGGGCCCACATGGA 1853 OY 1794 ATCGAGAAAACCATCTCCAAAAGGTGGGAACCGGGGGGGTATGAGGGCCACATGGA 1887 OY 1794 ATCGAGAAAAACCATCTCCAAAAACCAGGGGGACCCGGGGGGGG	1854 CAGAGGCGGGTCGGCCCACCCTCTGGCACCCTGTGCCCTGTGCCCTGTGCCCTGTGCCCTGTGCCCTGTGCCCTGTGCCGGGAGTGACGTTGTGCCTGTGCCCTGGGAGTGACGTTGTGACGTTGACGGAGAGATGACGTGCGGGGGGGG	~ ~~	Oy 2014 [OY 2154 GGGGAACGTCTTTCATGCTATGCATGCACACACACACACA	RESULT 8 -10-153-382-2 US-10-153-382-2 Sequence 2, Application US/10153382 Sequence 2, Application US/10153382 Sequence 2, Application US/1015381 Sequence 2, Application US/1015381 Sequence 2, Application US/1015381 Sequence 2, Application US/1015381 Sequence 3, Application US/10153382 Sequence 3, Application US/10153382 Sequence 3, Application US/10153382	FITTLE OF LINCE: PC23019A : US/10/153,382 FILE REFERENCE: 2019A : 2002-05-22 CURRENT APPLICATION NUMBER: 60/293042 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: 60/293042 NUMBER OF BEQ ID NOS: 39 NUMBER OF BEC ID NOS: 20 SOFTWARE: PRICETIN Ver. 2.1	DB	/v.*, pred. No. v. 6; Indersive 6; Namarches

us-09-627-896b-23.rnpb	SEQUENCE CHARD LINE LENGH: 2 TYPE: no. STRANDEDN MOLECULE TYPE: 15.10-027-075-29 Guery Mach. Best Local Similar	Match	23	Db		Oy 1147 GCACAGGCTCAGGGANGHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db
Oy 1732 AGGACTGGCTGAACGCCAAGTCAAGTCCAAGTCCAAGTCAAGTCAAGTCCAAGTCAAGTCAAGTCAAGTCCAAGTCAAG	1792 CCATCGAGANACCATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA			NUMBER OF SEQUENCES, 32 CORRESPONDENCES, 32 ADDRESSEE: 124170E ADDRESSE: 124170E COCKPIELD STREET: 60 State Street, suite 510 CONTY: Boston CONTY: Massachusetts CONTYE: NGSACHUSETE CONTYES READBLES FORM: CONTYES READBLES FORM: COMPINER READBLES FORM: COMPINER READBLES FORM:	OPERATING SYSTEM COMMELTING SOFTWARE: PATENCY OF WAS SOFTWARE SOFTWARE: PATENCY OF SOFTWARE:	NAME: AND ENVENTION: REGISTRATION: RESPERENCE/DOCKET NUMBER: 35.207 TELECOMMUNICATION INDERES: 42.207 TELEPHONE: (617) 227-5941	

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TITLE OF INVENTION: AND BACTERIAL DISEASES,
FILE REFERENCE. 030905.0004.CIP.
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR PILING DATE: 2000-04-28
NUMBER OF SEC ID NOS: 101
SOFTWARE: PALENTIN VOY: 2.1
                                                                                                                                                                                                                                                             Score 1547.2;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 94.1%;
Matches 1711; Conservative
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US-10-047-542-54
                                                                                                                                                                                LENGTH: 2009
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KEITH L.
NOVEL IMMUNOADHESINS FOR TREATING AND FREVENTING VIRAL
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US-10-047-542-54
US-10-047-542-54
; Sequence 54, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESI
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3	CTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACGGTCTCCTCAGGTGACTTACTCACGTCTCCTCAGGTGAGTCCTT	% q	1439 ATCCAGGGACAGCCCCAGCTGGGTGCTCACACGTCCATCTCTTCCTCAGCACC 1498
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a .	CIGGACCCIGCCTGGACCCICGTGGAIAGACAAAAACCGAGGGGCCICTGCGCCCTGGGC 60	. 6 0	1616 GGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG 1675
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1 & A	TCTGACCAGGGGGTGCACCTTCCCACTGCTACAGTCTCAGGACTCTACTCCT 84 TCTGACCAGGGGGTGCACCTTCCCACTGTCCTACAGTCCTCAGGACTCTACTCCCT 84 CCTGACCAGGGGGTGCACACTTCCCGGGTTGTCCTACAGTCTCTCAGGACTCTACTCCCT 61	Qy Dp	1856 GAGGCCGGCTCGGCCACCTTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTA 1915
oy Oy	CAGCAGCGTGGTCGACCGTCCACCAACTTCGGCACCCAACCTACACCTTCGAACGTTCGCAACGACCTACAACGTTCGAACGTTCGGCAACCTACAACGTTCGAACGTCTCGAACGTTCGAACGAA	ò da	1916 CAGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA 1975
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LOCATION: (1295) (1624) FATURE: NAME/KEY: mat peptide LOCATION: (1722) (2042) FATURE: LOCATION: (27) (2042) FEATURE: LOCATION: (27) (740) FEATURE: LOCATION: (27) (740) LOCATION: (21) (1106) LOCATION: (1132) (1176)	WARFIGNED 1929). (1624) 1624 1624 1624 1625
Qy 2096 CCGACGGCTCCTTCTTCTCTTACAGCAAGCTCACCGTGGACAAGAGCAGCAGCAGG 2155 Db 1894 CCGACGGCTCCTTCTTCTTTCTTTTTTTTTTTTTTTTTT	REBUIT 12 GENERAL TIE (1964 Application US/10216494 GENERAL TROMANGOZGO 20103976A1 APPLICANT: Serricans, NG US200103976A1LUSA APPLICANT: Serricans, Hiddynuk APPLICANT: Serricans, Hiddynuk APPLICANT: GENERAL TROMANGOZGO 2010 AD ACH LOOGISE CURRENT PRINCE 1001, ACH LOOGISE CURRENT APPLICANTON NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION NUMBER: US/00/49, 662 PRIOR APPLICATION: GENERAL US/00/49, 662 PRIOR APPLICATI

Qy 1856 GAGGCCGGCTCGGCCCACCCTCGGGAGTGACCGCTGTGCCCTATGTCCCTA 1915 bb 1660 GAGGCCGGCTCGGCCCACCCTCGGCGAGTGACCGCTGTACCAACCTCTGTCCCTA 1719 Qy 1916 CAGGGCAGCCCCCCACCTCTGCCCTGCCCCATCCCGGGAGGAGTGACCA 1975 Db 1720 CAGGCCAGCCCCGAGAACCACAGTGTACACCCTGCCCCATCCCGGGAGGAGTGACCA 1779 Qy 1976 AGAACCAGGTCAGCCTGCTGGTCAAAGCTTCTACCCCAGCGACATCCCGTGG 2035 Db 1780 AGAACCAGGTCAACCTGCTGGTCAAAGCTTCTACCCCAGCGACATCGCTGG 1839 Qy 2036 AGTGGGAGCACCTGACCTGGTCAAAGACTTCTACCCCAGCGACATCGCTGGTG 1899 Qy 2036 AGTGGGAGACCTGACCTGGTCAAAGACTACAAGACCACCCTCCCT	RESULT 13 US-10-144-142 Sequence 142, Application US/10216484 Sequence 142, Application US/10216484 Sequence 142, Application US/10216484 Sequence 142, Application US/10216484 Sequence 142, Application US/10216484 APPLICANT: Setziawa, No. US20030103976Alufuea APPLICANT: Haruyama, Hiddyuki APPLICANT: Tamaki, Irba APPLICANT: Tamaki, Irba APPLICANT: Tamaki, Irba APPLICANT: Tamaki, Irba APPLICANT: Tamaki, Irba APPLICANT: Tamaki, Irba APPLICANT: Tamaki, Irba APPLICANT: Tamaki, Irba APPLICANT: Tamaki, Irba APPLICANT: Tamaki, Irba APPLICANT: APPLICANTON NUMBER: US/10/216,484 CURRENT APPLICANTON NUMBER: US 002-08-09 SERIOR APPLICANTON NUMBER: US 09/083,583 FRIOR PILING DATE: 2000-02-09 SERIOR PLING DATE: AD00-02-09 SERIOR PLING DATE: AD00-02-09 SERIOR PLING DATE: AD00-02-09 SERIOR APPLICANTON NUMBER: US 09/083,583 FRIOR PLING DATE: AD00-02-09 SERIOR APPLICANTON NUMBER: US 09/083,583 SERIOR SELING DATE: AD00-02-09 SERIOR SELING DATE: AD00-02-09 SERIOR SELING DATE: AD00-02-09 SERIOR SERIOR APPLICANTON: ALIBED COTHER INFORMATION
788 TCTGACCAGCGGCGTGCACCTTCCCAGCTGTCCTACAGGACTCTACTCCCT 847 581 CCTGACCAGCGCGCACACCTTCCCAGCTGTCCTACAGGACTCTACTCCCT 640 6848 CCTGACCAGCGCGCCCCCCCCAGCTGTCCTCAGGACTCTACTCCCT 640 641 CAGCAGCGTGACCCTCCCAGCAACTTCGGCACCTACACCTGCAACGT 907 641 CAGCAGCGTGGCCGTGCCCTCCAGCAACTTCGGCACCTACACTTGCAACGT 700 908 AGATCACAAGCCCAGCAACACCCAGGCACACAGACACTTGCAACGT 700 908 AGATCACAAGCCCAGCAACACCCAGGGAACACACTGCAACGT 700 908 AGATCACAAGCCCAGCAACACCAAGGTGACAAGAGAGCCACACACGCAACGT 700 908 AGATCACAAGCCCAGCAACACCCAAGGTGACAAGAGAGAG	1208 CCTGCCDAAAGCCATATCCGGGAGGACCCTGCCCTGACCTAAGCCCACCCCAAGGCCA 1267 1000 CCTGCCCAGGGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCCAAGGCCA 1059 1000 CCTGCCAGGAGCCCTTGCTCCTCCCCCCGAGCCTAAGCCCCACCCCCAAGGCCA 1059 1000 AACTCTCCCTCAGCTCGGACCTTCCTCTCCTCCCCCCAAGTCCCATAT 131 1120 CTTCTCTCTCTCGCAGCCCCAATCTTCTTGTGCCACCCTGCCCAGGT 1179 1120 CTTCTCTCTCTCAAGCGCCAATCTTGTGTCACACTCTCCTCCACCTGCCCAGGT 1179 1120 CTTCTCTCTCGCAGCCCCCAGCTCAGCCCCCCAGGTCACTCCCTCC

Qy 548 CTGGACCCTGGCTGGACCCTCGTGGATAGACAGAACCGAGGGCCTCTGCGCCCTGGGC 607 Db 407	Qy 668 CCCATCGGTCTTCCCCTGGCGCCTGCTCCAGAGCACCTCCGAGAGCACAGCGCCCT 727 bb 457 CCCATCGGTCTTCCCCTGGCACCTCCTCCAAGAGCACTCTGGGGGCACAGCGGCCT 516 Qy 728 GGGCTGCTGGTCAAGACACTTCCCCGAACCGGTGACGGTGTGGAACTCAGGGG 787 Db 517 GGCTGCTGGTCAAGAACTACTTCCCCGAACCGGTGACGGTGTGGAACTCAGGGGC 786	188 TCTGACCAGGGGGGGGCACCTTCCCAGCTGTCCTACAGTCTCAGGACTCTACTCCCT -	908 697 968	Oy 1028 CAGCCCCAGCCCAGGCAGCAGGCCCCATCTGTCTCCTCACCGGAGGCCTCTGC 1087	1148 CACAGGCTGGGTGCCCTACCCCTTCACACAGGGGGGGGGG	1268 A 1056 A 1328 C	OY 1379 AAGCCAGGCCTCGCCTCCAGGCTCAAGGCGGACAGTGCCTAAAGTAGCTGC 1438 1176 AAGCCAGGCCTCGCCTCCAGCTCAAGGCGGGACAGGTGCCTAAGATAGCCTGC 1235 OY 1439 ATCCAGGACAGGCCTCGAGTGCTGACAGTCCACCTCATCTCTCTC	
LOCATION: (1128)(1172) PEATURE: NAME/KEY: exon LOCATION: (1291)(1620) PEATURE: NAME/KEY: exon LOCATION: (1718)(2038)		LOCATION: (1291) (1620) PEATURE: NAME/KEX: mat peptide LOCATION: (1718) (2038) PEATURE: NAME/KEY: CDS LOCATION: (2038) LOCATION: (2038) PEATURE: PEATURE: PEATURE:	NAME/KEY: CDS LOCATION: (1128)(1172) PEATURE: NAME/KEY: CDS CCATICN: (1291)(1620) FEATURE: NAME/KEY: CDS NAME/KEY: CDS LOCATION: (1718)(2038)	US-10-216-484-142 Query Match Best Local Similarity 81.9%; Score 1455.4; DB 15; Length 2073; Best Local Similarity 81.9%; Pred. No. 0; Matches 1843; Conservative 0; Mismatches 171; Indels 235; Gaps 5; Qy 8 CACARGGGAGGAGGAACATACATCTTTCTTTCTTCTTCTTCTTCTTCTTCTTCT	Db	139 GTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGGGTGGG	259 CAATCAAAAGTTCAAGGGCAAGGTTGACTGTAGACATCCACTAGGACAGCCTA 308 TATGAAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGC 319 CATGGAACTTAGAGATCTGAGATCTGAGGACACGCGTTTATTACTGTGCAAGAGCGGC 319 CATGGAGCTCAGCAGCATGAGACTCGAGGACACGGGCGTTATTACTGTGCAAGAAATAG 368 CAGGTATATGGACTACTGGGGTACAAGGTACCCTTGTCAGGTGAAGTAGTTACTGTATACTGTAGAAGAAAATAG 1111 111 111 111 111 111 111 111 111 1	Db 379 GGACTATAGTAACAACTGGTACTTCGAT

	### 1737. (1237) ### 1737. (1237) ### 1737. (1238) ### 17
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; PRIOR APFLICATION NUMBER: US/09/499,662 ; PRIOR FILING DATE: 2000-02-09	qa	83 TCAGGTCCAACTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGGCTTCAGTGAAGGT 142
PRIOR APPLICATION NUME PRIOR FILING DATE: 199	ò	128 GICCIGCAAAGCIICCGGCIACACAIICACIGAIIAIGCIAIACAGIGGGIGAGACAGGC 187
Ø	qq	143 GTCCTGCAAGGCTTCTGCCTACACCTTCACCAGCAACGAAGGGGTACGACAGGC 202
LENGTH: 2077	۸٥	188 TCCTGGACAGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAAACTA 247
	qq	203 CCCTGGACAGGGCCTTGAGTGGATGGGAGAGATTGATCCTTCTGATAGCTATACTAACTA
NAME/KEY: sig peptide; LOCATION: (27). (83)	ò	248 CAACCAGAAGTITAAGGGCAAGGCCACAATGACTGTAGAAGTCGACGAGCAGCCTA 307
FEATURE: NAME/KEY: intron	qa g	CAATCAAAGGTCCGGGTCACAATCACTCGAGACACATCCACTAGCACAGACACCTA
intron	승 옵	308 ATGGARCITAGILLITIEAGAICIGAGGAIACCAGCCCGTTATIACIGCGAGGGGCGGGC 387
	ò	368 CTGGTAȚATGGACTACȚGGGGTCAAGGTACCCTTGTCACGTCTCCTCAGGTGAGTCCTT 427
; NAME/KEY: intron ; LOCATION: (1625)(1725) : FEATURE:	q _Q	383 GGACTATAGTAACAACTGG
NAME/KEY: exon; LOCATION: (27)(740)	ò	AAAAC
; FEATURE: NAME(KEY: exon ; LOCATION: (1132)(1176)	අ ඊ	402TACTTCGATGTCTGGGGCGAAGGGACCCTGGT
exon	, qa	434 433
	٥٨	548 CTGGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGC 607
) MANUAL AET: EXOII LOCATION: (1722)(2042)	qq	434 433
NAME/KEY: mar peptide ; LOCATION: (84).(740)	ò	608 CCAGCTCTGTCCCACACCGCGGTCACATGGCACCTCTTTTGCAGCCTCCACCAAGGG 667
	qu	434CACCGTCTCCTCAGCCTCACCAAGGG 460
(1)	ò	668 CCCATCGGTCTTCCCCCTGGCCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCT 727
; NAME/KEY: mat peptide ; LOCATION: (1295)(1624)	අු	cccarcestricccccrescacctccrccaasascaccrtrssscacacacacacaccr
FEATURE: NAME/KEY: mat peptide COATION: (1722)(2042)	& a	728 GGGCTGCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGGGAACTCAGGCGC 787
) FEATURE: NAME/KEY: LOCATION: (27)(740)	۸۵	788 TCTGACCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTCCCT 847
CDS	qa	581 CCTGACCAGCGGCGTGCACACTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT 640
(1132) CDS	ò a	848 CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGT 907
_	oy.	agatcacaagcccagcaacaccaaggtggacaagacagttggtgagagggccagctcaggg
10N: (1722)(2042)	ପ୍ର	GAATCACAAGCCCAGGAACACCAAGGTGGACAAGAGATTGGTGAGAGGCCAGCACAGGG
) UTHER INFORMATION: DESCRIPTION OF ATTITIONAL Sequence: Designed DNA; OTHER INFORMATION: encoding the heavy chain of humanized anti-Fas; OTHER INFORMATION: antibody US-10-216-484-156	ò a	968 AGGAGGGTCTGCTGGTGGGTCAGGCTCAGCCTCCTGCTGGACGCACCCGGGTGTG 1027
	oy Bb	1028 CAGCCCCAGCCCAGGGCAGCAGCAGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGC 1087
ACCATGGGTTGGAACTGTATCATCTTTTTCTGGTTACCACAGCTACA	γ d	1088 CCGCCCCACTCATGCTCAGGGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGG
23	8 8	CACAGACTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCACA
Oy 68 CCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT 127	금	

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Search completed: July 18, 2003, 15:38:36 Job time: 554.679 secs

	1208	CCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCA 126	69
	1268	AACTGTCCACTCCCTCAGGTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAAT 132	
	1328	CTTCTCTCTGCAGAGGCAAATGTTGTGGAGTGCCCACCGTGCCCAGGT 137	8.
	1379	AGGG	. 8 6
	1439	ATCCAGGGACAGGCCCAGCTGGGTGCTGACACGTCCACCTCCATCTTCCTCAGGACC 149	86
	1499	CCCTCAT 15	55
	1556	GATCTCCCGGACCCTGAGGTCACGTGCGTGGTGGAGACGTGAGCCCACGAAGACCCCGA 161	. 61
	1616	GGTCCAGTTCAACTGGTACGTCGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG 167 	
	.1676	GGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGA 173	35
	1736	CTGGCTGAACGCCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCAT 179	
	1796	CGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGGGGGTATGAGGGCCACATGGACA 185 	
	1856	GACCGCTGT GACCGCTGT	· 6]
	1916	CAGGGCAGCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGGGGGAGATGACA 197	
	1976	20	
	2036	AGTGGGAGAGCAATGGGCAGCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACT 209	
	2096	21	
•	2156	GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACCACGCAGAAGA 221	
	2216, 2020	GCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244	

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Patent NO. 5871732

GENERAL INDEMATION:
APPLICANT: CHISHOLM, PARFICIA L.
APPLICANT: THOWAS, DAVID W.
APPLICANT: THOWAS, DAVID W.
APPLICANT: THOWAS, DAVID W.
APPLICANT: THOWAS, DAVID W.
APPLICANT: THOWAS, DAVID W.
APPLICANT: ROSA, JOSEPH D.
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APPLICANT: ROSA, JOSEPH D.
APPLICANT: CHICAGO
COUNTRY: U.S.A.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ADDRESSEE: FLORY disk.
ADDRESSEE: FLORY MACKER DRIVE
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
ACMINICANT FLORY
COMPUTER READABLE FORM:
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Sequence 418
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MEDIUM TYPE: Floopy disk
MEDIUM TYPE: Floopy disk
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
SOFTWARE: 18M PC compatible
SOFTWARE: 18M PC compatible
COMPUTER: 18M PC compatible
SOFTWARE: 18M C compatible
APPLICATION NUMBER: 18/07/916,098A
FILING DATE: 011/19 compatible
REPERTING DATE: 018/07/916,098A
CLASSIFICATION DATE: 02/91/132ember 27, 1991
FILING DATE: 08/81/132ember 27, 1991
FILING DATE: 08/81/132ember 27, 1990
FILING DATE: 08/81/132ember 27, 1990
FILING DATE: 08/81/132ember 27, 1990
APPLICATION NUMBER: 26/949
ILASSIFICATION NUMBER: 26/949
NAME: JOHN J. NC DONNELL
NAME: JOHN J. NC DONNELL
NAME: JOHN J. NC DONNELL
NAME: JOHN J. NC DONNELL
REFERENCE/DOCKET NUMBER: 92,310-G
REFERENCE/DOCKET NUMBER: 92,310-G
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                                                                                                      ZIP: 02210-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BAC COMPATIBLE
COMPUTER: BAC COMPATIBLE
COMPUTER: BAC COMPATIBLE
COMPUTER: BAC COMPATIBLE
CONSTRAING SYSTEM: PC-DOS/NS-DOS
SOCTWARE: PAPELICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
FILING DATE:
FLING DATE: US 60/000,213
FILING DATE: US 60/000,213
FILING DATE: US 60/000,213
FILING DATE: US 60/000,213
CLASSIFICATION:
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89.1%; Pred. No. 0;
iive 0; Mismatches
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TELECOMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEFX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2287 base pairs
          225 Franklin Street
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NAME: Lech, Karen F.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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STRANDEDNESS: single
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Matches 2038; Conserv
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                                     Boston
                                                                                      USA
                                CITY: BOS
STATE: MA
COUNTRY:
ZIP: 022
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PCT-US96-10043-8
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                        CCCTGCTCCAGGAGCACCTCCGAGAGCACCAGCGCCCTGGGCTGCCTGGTCAAGGACTAC
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Pred. No. 0;
0; Mismatches 219; Indels
APPLICATION NUMBER: US/08/480,036
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/618,314C
FILING DATE: No. 572563ember 23, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/067001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: (617) 542-5070
TELEFAK: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                73.48;
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Best Local Similarity 87.2
Matches 1998; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                            LENGTH: 2287
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                                                                                                               Length 2287;
                                                                                                             Ouery Match 73.4%; Score 1651.6; DB 1; Length Best Local Similarity 87.2%; Pred. No. 0; Matches 1998; Conservative 0; Mismatches 219; Indels
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2287
                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                      linear
                                                                       ; TOPOLOGY:
US-08-461-968A-1
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CCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA 1932
                                                       AAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCA 1872
                                                                       1846 AAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGCCCCA 1905
                                                                                                                            CCACAGGTGTACACCCTGCCCCCATCCCGGGAGAGATGACCAAGAACCAGGTCAGCCTG 1992
                                                                                                                                                                                                                                           ACCTGCCTGTCAAAGGCTTCTATCCCAGCGACATGGCCGTGGAGGTGGGAGAGAGCAATGGG 2084
                                                                                                                                                                                                                                                                                                CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC 2144
                                                                                                                                                                                                                                                                                                                                      CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGAGCAGCAGGGGAACGTCTTCTCATGC 2172
                                                                                                                                                                                                                                                                                                                                                       2145 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTCTCATGC 2204
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                                                                                                                                                                                                                                                                              CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTC
                                                                                                                                                                                       1965 CCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTG
                                                                                                                                                                                                                          1993 ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAAATGGG
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US-08-461-968A-1
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1110 GAGGGTCTTCTGGCTTTTTCCACCAGGCAGGCAGGCTAGGTGCCCCTACCC	1290 GACACCTTCTCCTCCCAGATAACTCCCAATCTTCTCTGCAGAGCGCAAAT	1401 CCAGCTCAAGGCGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGACAGGCCCCAGCTG 1460 1431 CCAGCTCAAGGCGGAACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCG 1490 1461 GGTGCTGACAGCTCCACCTCTTCCTCAGCACCACCTGCGGCAGCACGTCA 1517 1461 GGTGCTGACAGCTCCACCTCTTCTCTCAGCACCCACCTGCGGCAGCACCGTCA 1517 1461 GGTGCTGACACCTCCACCTCTTCTTCTTCAGCACACCGCAGACACCGTCA 1510 1461 GGTGCTGACACCTCCACCTCCATCTCTTCTTCTAGCACACACGGCAGACCGTCA 1550	518 GTCTTCCTCTTCCCCCCAAAACCCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 157	2000	93 GCACGTTCCGTGTCGGCGTCCTCCCCGTGTGCCCCGGGACTGGCTGACGGCAAGG 175	1753 AGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCATCGAGAAACCATCTCCA 1812		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG 199	93 ACCTGCCTGGTCAAAGGCTTCTACCCCAGGACATCGCCGTGGAGTGGAGTGCAATGG 1	S CAGCCGGAGAACAACTACAAGACCACGCCTCCGTGCTCGGACTCCGACGGCTCTTTTC 214	2113 CTCTACAGGTTCACCGTGGACAAGCTGGCGGGGGGGGAAGCTTTCTTGC 2172 2145 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCGGGAACGTCTTCTCATGC 2204
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7 ACCACCATGGACTGGAGGTTCCTCTTTTGTGGTGGCAGCAGCTACAGGTGTC 66 63 CACTCCCAGGTCCAGCTGGAGGTTCCTCTTTTGTGGTGGCAGCTACAGGTGTC 122	AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACCACAACAACAAGAAAAAAAA	307 GCGG	427 CAGGGAACCTGGTCACCGTCTTCAGGTGAGTACTGAATTCTAGCTTTCTGGG 481 450 GCGAGCCGGGCCTGACTTTGGGCTTTTGGGCAGGGAGTGGGCTAAGGTGAGGCAGGGGGG 509	510 CCAGCCAGGTGCACACCCAATGCCCGGAGCACCAGGACCCTGCCTG	596 CGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGGCCCAGCTCTGTCCCCACCCCGGG 554 630 TCACATGGCACCACTCTTGCAGCCTCCACCAAGGGCCCATTGGTCTCCCCCTGGGG 689 [90 CCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC	TTCCCGGAACCGGTGACGGTGCGGGAACTCGGCGCTCTGACCAGCGCGTGCACCGGGGCGTGCACCGGGGCGTGCACCGGGGGGGG	835 TICCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 894 870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAAGTCACAAGCCCAGGAACAC 929 11	930 AAGGTGGACAAGACAGTGAGAGGCCAGCTCAGGGAGGGAG	990 CAGGCTCAGCCCTCCTGCACGCACCCCCGGCTGTGCAGCCCCAGCCCAGGCAGCAA 1049	1050 GGCAGGCCCCATCTGTCTCCTCACCCGAGGCCTCTGCCCGCCC

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303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362
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                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 370:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1611.8;
Pred. No. 0;
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                                                                       WO PCT/US96/16433
                                                                                                                                                                                                                                                           WO PCT/US97/21803
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/1643
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/2180
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAMME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.3%;
Matches 1722; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4723 base pairs
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STRANDEDNESS: sing
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US-09-042-353-370
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2173 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCG
                                                                       2205 TCCGTGATGCATGAGGCTCTGCACACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA.
PEDLICATION UNDER: US/09/042,353
FILING DATE: 13-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR DATE: 18-WAK-1992

PRIOR APPLICATION DATA: 1992

PILING DATE: 23-UN-1992

PRIOR APPLICATION DATA: 07/904,068

PILING DATE: 23-UN-1992

PRIOR APPLICATION DATA: 07/990,860

FILING DATE: 16-DEC-1992

PRIOR APPLICATION DATA: 08/053,131

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/096,762

FILING DATE: 26-APR-1993

PRIOR APPLICATION NUMBER: US 08/155,301

FILING DATE: 18-NOV-1993

PRIOR APPLICATION NUMBER: US 08/155,301

FILING DATE: 18-NOV-1993

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/155,301

FILING DATE: 18-NOV-1993

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/155,301

FILING DATE: 18-NOV-1993

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICAT
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PRIOR APPLICATION DATA:
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/810,279
PRIOR APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729 ACT
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10-DEC-1993
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13-MAR-1998
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COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         US-09-042-353-370
; Sequence 370, Application US/09042353
Patent No. 6255458
; GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
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                                                                                                                                     2244
                                                                                                                                                                                             2265 GGTAATGAGTG 2276
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CITY: San Francisco
STATE: California
COUNTRY: USA
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PRIOR APPLICATION DATA:
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Gaps

10 ACCTICATOR CONSECUENCY 1.10 Bot 4; Length 4721;			Qy 1918 GGGCAGCCCCGAGAACCACAGGTGACACCCCCCCCTCCCGGGAGGAGATGACCAAG 1977 Db 1502 GGCCAGCCCCGAGAACCACAGGTGACCCCCCCCCCCCCC	RESULT 8 US-07-916-098A-43 US-07-916-098A-43 US-07-916-098A-43 Sequence 43, Application US/07916098A Patent No. 581732 GENERAL INFORMATION: APPLICANT: BUKKLY, LINDA C. APPLICANT: CHISHOLM, PATRICIA L. APPLICANT: THOMAS, DAVID W. APPLICANT: ROSA, WARGARET D. APPLICANT: ROSA, JOSEPH J. ITILE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN ITILE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION ITILE OF INVENTION: BROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION CORRESPONDENCE ADDRESS: ADDRESSEE: ALEGRETTI & WITCOFF, LTD. STREET: 10 SOUTH WACKER DRIVE CITY: CHICAGO
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28 28 28 28 28 28 28 28 28 28 28 28 28 2	### Pred: DB 4; Length 4723; ### Local Similarity	AGCTCTGTCCACACGCGGGTCACATGGCACCACTCTTTGTGTGTTTTGTGTTTTTGTTTTTGTTTTTTGTTTTTT		TGCCAAAAGCCATATCCGGAGGACCCTGCCCTGACCTAAGCCGACCCCAAAGGCCAAA [

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               ZIP: 60606
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION NUMBER: O7/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
APPLICATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
REGISTRATION NUMBER: 26,949
RECHERNICE/DOCKET NUMBER: 26,949
TELLECOMMUNICATION INFORMATION:
TELEPRONE: (312) 715-1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: binear TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO PEATURE: NO
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OY 1935 ACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAGGACCAGGTCAGCCTGAC 1994	Query Match 70.5%; Score 1584.6; DB 3; Length 2482; Best Local Similarity 99.7%; Pred. No. 0; Matches 1587; Conservative 0; Mismatches 4; Indels 0; Gaps 0
Qy 1995 CTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCGTGGAGAGAGA	Qy 654 GCCTCCACGAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 71.3 L
Qy 2055 GCCGGAGAACAACTACAAGACCACCCCCCATGCTGGACTCCGACGGCTCCTTCTTCCT 2114	Qy 714 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773 1
Qy 2115 CTACAGCTAAGCTCACCGTGGACAAGAGCAGCAGCAGCGGAACGTCTTCTCATGCTC 2174 Db	Qy 774 TGGBACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833 bb 808 TGGBACTCAGGCGTCTGACCAGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867
Qy 2175 CGTGATGCATGAGGTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCGGG 2234	Qy 834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893 bb 868 GGACTCTACTCCCTCAGCAGCGTGGTACCCTCCAGCAACTTCGGCACCCAGACC 927
Oy 2235 TAAATGAGTG 2244 Db 1799 TAAATGAGTG 1808	Oy 894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACGTGGACAAGACAGTTGGTGAG 953
RESULT 9 US-08-477-460B-3 Sensence 3 banlication RE/08477460B	Qy 954 AGGCCAGCTCAGGGAGGGAGGTGTCTGCTGGAAGCCAGCC
Fatent No. 603423 GENERAL INFORMATION: APPLICANT: Progenics Pharmaceuticals, Inc.	QY 1014 GCACCCCGGCTGTGCAGCCCCAGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGC
1111B OF INVENTION: NON-PERILITY MOLETY-CONDUCATES, AND USES THEREOF; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF; NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSED OF CONDUCE ADDRESS:	Oy 1074 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGAGAGGTCTTCTGGCTTTTTCCACC 1133
STREET: 30 Rockefeller Plaza CITY: New York STATE: New York	Qy 1134 AGGCTCCAGGCAGCCAGGCTGGCTGCCCTACCCCAGGCCCTTCACACACA
ZIP: 10112 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	Qy 1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCTGACCTTGAGCC 1253 L228 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTTAAGCC 1287
COMPEDIATION SYSTEM: PC-DOS/MS-DOS CORTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:	Oy 1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGGTCGGACACCTTCTCCTCCTCCACATCC 1313 [
AFFLICATION NUMBER: 05/08/47/480B ; FILING DATE: 07-JUN-1995 ; CLASSIFICATION: 530 ; PRIOR APPLICATION DATA:	Qy 1314 GAGTAACTCCCCAATCTTCTCTGCACACGCAAATGTTGTGTGGGGGGGCCCACCGTGCC 1373
	Qy 1374 CAGGTAAGCCAAGCCTAGGCTCCAGGTCCAAGGGGGACAGGTGCCCTAGAGTAG 1433 L408 CAGGTAAGCCACCCAAGGCTCCAGCTCCAGGTCAAGGCGGACAGGTGCCCTAGAGTAG 1467
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:	Oy 1434 CCTGCATCCAGGAAAGCCCCAGCTGCTGCTGACACGTCCACCTCCATCTTCCTCA 1493
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: 1. ENGTH. 2462 has a paint	Oy 1494 GCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCTC 1553
TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: unknown MAISTRIE TYPE: ACID TO TO TO TO TO TO TO TO TO TO TO TO TO	Oy 1554 ATGATCTCCCGGACCCCTGAGGTCACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG
C	0y 1614 GAGGTCCAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1673
US-US-4//-400B-3	Qy 1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1733

us-09-627-896b-23.rni

	834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGGACC 893	894 TACACCTGCAACGTAGATCACAAGCCCAGGAACACCAAGGTGGACAAGACAGTTGGTGAG 953 	954 AGGCCAGGTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCCTCAGCCTCCTGCCTG	1014 GCACCCGGGTGTGCAGCCCCAGGGCAGCAAGAGGCAGGCCCATCTGTCTCCTCAC 1073	1074 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGGGTCTTCTGGCTTTTTCCACC 1133	1134 AGGCTCCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACA	1194 GIGGITGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCCGGCCCCTGACCTAAGCC 1253 1228 GIGCITGGCTCAGACCTGCCAAAAGCCATATCCGGAAGAACCCTGCCCCTGACCTAAGCC 1287	1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGATCGGACACCTTCTCTCCTCCCCCCAGATCC 1313	1314 GAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGGAGTGCCCACCGTGCC 1373	1374 CAGGTAAGCCAGGCCTGGCCTCCAGCTCAAGGGGGGACAGGTGCCCTAGAGTAG 1433	1434 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTCACCACCACCACCTCTTCTTCTCT 1493	1494 GCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1553	1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGGCGCGGAGGCCACGAAGACCCC 1613	1614 GAGGTCCAGTTCAACTGGACGTGGAGGTGCATAATGCCAAGACAAAGCCA 1673 	1674 CGGGAGGACCAGTTCAACAGCACGTTCCGTGTGGTCCAGCGTCCTCACCGTTGTGCACCAG 1733	1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGCTCCCAACAAAGGCCTCCCAGCCCC 1793	1794 ATCGAGAAAACCATCTCCAAAACCAAGGGGGCCGGGGGTATGAGGGCCACATGGA 1853
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	QY 1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGGGGGGGTATGAGGGCCACATGGA 1853 Db 1828 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGGGGGGTATGAGGGCCACATGGA 1887	0y 1854 CAGAGGCCGGCTCGGCCCTCTGCCCTGGGAGTGACGCTGTGCCAACCTCTGTCCC 1913	OY 1914 TACAGGGCAGCCCCAAQAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGAGATGAC 1973	OY 1974 CAAGAACCAGGTCAGCTGACCTGGTCAAAGGCTTCTACCCCAGGACATCGCCGT 2033	OY 2034 GGAGTGGGAGGCAGCGGGAGAACAACTACAAGACCACCTCCCATGCTGGA 2093	OY 2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAGCTCACCGTGGACAGAGCAGGTGGCAGCA 2153	OY 2154 GGGGAACGTCTTCTCATGCTCCGTGATGAGGCTCTGCACACACTACACGCGAAA 2213	Oy 2214 GAGCCTCTCCCGGGGTAAATGAGTG 2244	RESULT 10 US-08-379-516-3	; Sequence 3, Application us/083/9216; Patent No. 6083478; GENERAL INFORMATION: APPLICANT Allaway, Graham P.	TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2; TITLE OF INVENTION: Immunoconjugates and Uses Thereof FILE REPERENCE: 41215-4-ECT-US FILE REPERENCE: 41215-4-ECT-US FILE REPERENCE: 41215-4-ECT-US	CURRENT FILING DATE: 1996-06-10 ; EARLIER APPLICATION NUMBER: PCT/US93/07422 ; EARLIER AILING DATE: 1993-08-06 ; EARLIER PLING DATE: 1993-08-06 . EARLIER DADITON ANTHERDED: 07/07/07	FARLIER FILING DATE: 1992-08-07; BARLIER FILING DATE: 1992-08-07; NUMBER OF SEQ ID NOS: 9; SOFFWARE: Patentin Ver. 2.1	; LENGTH: 2482 ; TYPE: DNA ; TYPE: DNA ; GRANISM: Homo sapiens	Ouery Match 70.5%; Score 1584.6; DB 3; Length 2482; Best Local Similarity 99.7%; Pred, No. 0; Marchae 1687. Concernsting or Marchae 1687.	654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCTCCAGGAGCACCTCCCAG 71	UD 688 GCCTCCACCAAGAGCCCATCGGTCTTCCCCCTGGCGCCCTGCTGCAAGAGCACTCCGGA 747 Qy 714 AGCACAGGGGCCCTGGGTGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773

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23-627-896b-23	1913 1947 1973 1973 1973 1 2007 1 2007 1 2007 1 2007 1 2007 1 2007 1 2012 1 2067 1 206	TITLE OF INVENTION: CUATORS OF SEQUENCES: 9 NUMBER OF SEQUENCES: 9 NUMBER OF SEQUENCES: 9 NUMBER OF SEQUENCES: 9 NUMBER OF SEQUENCES: 9 NUMBER OF SEQUENCES: 9 NUMBER OF SEQUENCES: 9 OF SEQUENCES: 0 ROCKETLET PLANCE OF SECUENCES CONTYN: New York CITY: New York CITY: New York CITY: New York COMPUTER: PLORPY disk COMPUTER: PLORPY DISK: 09/329,916 COMPUTER: PLORPY DEATH OF PLANCE OF SECUENCES COMPUTER: 18M PC PC_DOS/NOS 09/329,916 CUBERATING PARTION DATE: 09/329,916 PILING DATE: CLASSPLICATION DATE: 09/329,916 PILING DATE: CLASSPLICATION NUMBER: US 0/7927,931 PILING DATE: NEW NUMBER: US 0/7927,931 PILING DATE: NUMBER: US 0/7929,916 APPLICATION NUMBER: US 0/7929,916 ATTORNEY AGENT INFORMATION: REFERENCICATION RIPORMATION: REPRESENTATION REPRESENTED RIPORMATION: REPRESENTATION REPRESENTED RIPORMATION: REPRESENTATION REPRESENTED RIPORMATION: REPRESENTED REPRESENTED RIPORMATION: REPRESENTED REPRESENTED RIPORMATION: REPRESENTED REPRESENTED

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	Oy 2034 GAGAGGGAGGCAGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGGGGG	GENERAL INFORMATION APPLICANT: MEDICAN APPLICANT: MEDICAN TITLE OF INFORMATION: Cary A TITLE OF INFORMATION: Cary A NUMBER OF SEQUENCES: CORRESSED ADDRESS: ADDRESSED COOPER & DUNHAM LLP STREET: New York COUNTRY: USA CONDITY: USA CONDITY: 185 APPLICAS CONDITY: 1036 MEDIUM TYPE: FLORM: COMPUTER: TRABET STREET:	APPLICATION DATA: BESSE #1.24 FILING DATE: US/08/485,372A CLASSIFIÇATION: 435

1314 GAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCC 1373

ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: USA ZONTRY: USA MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: COMPUTER: IBM PC Compatible	CURRENT NO SYSTEM: PC-DOS/MN-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/409,006A FILING DATE: 29-SEP-1999 CLASSIFICATION DATA: PRIOR APPLICATION DATA: APPLICATION OF SYSTEM	FILING DATE: 07-AUG-1992 ATTORNEY/AGENT INFORMATION: NAME: White, John P. REGISTRATION NUMBER: 28,678 REFERRENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 977-9850	18 4 2 2 3 E E	; OKGANISM: homo sapien ; CELL TYPE: lymphocyte US-09-409-006A-3 Query Match 70.5%; Score 1584.6; DB 4; Length 2482; Best Local Similarity 99.7%; Pred. No. 0; Matches 1587; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Oy 654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCTGGGGCCCTCCAGGAGCACCTCCGAG 713	Qy 774 TGGAACTCAGGGGTCTGACCAGCGGGGGGGCGTGCACCTTCCCAGCTGTCCTACAGTCCTCA 833 Db 1000 B08 TGGAACTCAGGCGCTCTACCAGCGGCGTGCACCCTTCCCAGCTGTCCTACAGTCCTCA 867	0y 834 GAACTCTAACACAGAGCGTGGTGACCGTGCCCTCCAGAACTTCGGCACCCAGACC 893	Db 928 TACACCAGCAACATAGATCACCAGCAACACCAAGGTGGACAAGACGTGGAC 987
Db 13%8 GAGTAACTCCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTGGGTGCCCACCGTGCC 1407 Oy 1374 CAGGTAAGCCAGCCTCGCCTCCAGCTCAAGCGGGACAGGTGCCCTAGAGTAG 1433 Db 1408 CAGGTAAGCCAGGCCTCGCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1467 Oy 1434 CCTGCATCCAGGGACAGGCCCCAGGTGCTGACACGCTCCATCTTCCTCA 1493 Db 1468 CCTGCATCCAGGGACAGGCCCCAGGTGGTGCTGACACGTCCATCTTCTTCCTCA 1527	Oy 1494 GCACCACGGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAACCCAAGGACACCTC 1553	Qy 1614 GAGGTCCAGTTCAACTGGTACGTGGACGCGTGGAGGTGCTAAGCCAAGACAAAGCCA 1673 Db 1648 GAGGTCCAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1707 Qy 1674 CGGGAGGAGGTTCAACAGCACGTTCCGTGTGGTCCTCACCGTTGTGCACCAG 1733 Db 1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCCTCACCGTTGTGCACCAG 1767	1734 GACTGGCTGAACGGCAAGGACTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCCCC	1838 CAGAGGCGGCCCACCCTCTGCCTGGGGGTGACCTGTGCCCTGTGCCC	Qy 1974 CAAGAACCAGGTCAGCCTGACCTGGTCAAGGCTTCTACCCCAGGGACATGGCGGT 2033 Db 2008 CAAGAACCAGGTCAGCCTGGTCTGCTGGTCAAGGCTTCTACCCCAGCGACATGGCGT 2067 Qy 2034 GGAGTGGGAAATGGGCAGCCGGAGAACAACTACAAGACCACCTCCCATGCTGGA 2093 Db 2068 GGAGTGGGAAGCAATGGGCAGCCGGAAACAACACACACCTCCCATGCTGGA 2127	2094	Oy 2154 GGGAACGTCTTCTCATGCTCGTGATGCATGACCTCTCCACCACCACCAGAA 2213 Db 2188 GGGAACGTCTTCTCATGCTCGTGATGATGATGATGATCACACACA	Db 2248 ĠAĠCĊTĊŢĊŢĊŢĊŢĠŢĠŢĠŢĠĀĀĀŢĠĀĠŢĠ 2278 RESULT 13 US-09-409-006A-3 Sequence 3, Application US/09409006A Patent No. 634286 GENERAL INPORMATION APPLICANT: Progenics Pharmaceuticals, Inc. TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED TITLE OF INVENTION: C14-GAMMA2 AND C04-IgG2 IMMUNOCONJUGATES, AND USES THEREOF NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:

QY 2214 GAGCCTCTCCCGGGGTAAATGAGTG 2244 Db 2248 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2278	RESULT 14 US-08-484-681-3 Sequence 3, Application US/08484681 Setent No. 6451313 SENERAL INFORMATION: APPLICANT: Beaudry, Gary A. TITLE OF INVENTION: TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS	CORRESPONDENCE ADDRESS: 9 **ADPRESSE: Cooper & Dunham LLP **STREET: 1185 Avenue of the Americas CITY: New York **CUMPRY: USA	ZIP: 10036 COMPUTER REDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:	FILING DATE: US/08/484,681 FILING DATE: US/08/484,681 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: White, John P. REGISTRATION NUMBER: 28,678 TELECOMMUNICATION INFORMATION:	TELEPHONE: (212) 278-0400 TELEFAX: (212) 391-0525 TELEX: T	eic acid S: double unknown : cDNA CE: homo sapien	11-3 21-3	688 714 748		
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AL I GNMENTS

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AY043139 Homo sapi 200004 Human germl M23848 Human Ig re

AY043133 Homo sapi

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PRI 17-FEB-1993 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 327) X70459.1 GI:38436 anti-DNA antibody; complementarity determining region; Ig kappa light chain; Ig light chain; Ig variable region; IgM; immunoglobulin; systemic lupus erythematosus. אסס מאבאור PRI 1 H.sapiens DNA for anti-DNA antibody light chain variable region, subgroup V(K) I (III-2R IgM line). X70459 REFERENCE

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Hmman Ig kappa chain V-region (VL-COL) mRNA, partial cds.
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(bases 1 to 338)

Pritsch,O., Magnac,C., Dumas,G., Egile,C. and Dighiero,G.
V gene usage by seven hybrids derived from CD5+ B-cell chronic lymphocytic leukemia and displaying autoantibody activity 94033522
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Pritech, O., Magnac,C., Dumas,G., Egile,C. and Dighiero,G.
Direct Submission
Submitted (24.JAN-1997) Unite d'Immunohematologie et
d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris
75724, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTAGCCTGGTATCAGCAGAAACCA
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                                                                                                                                                                                product"
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/note="unnamed protein
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Homo sapiens
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                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/db xcre="taxon:9660"
/sub_clone="pathescript"
/cell_line="EBV-transformed 31(+) B cell line III-2R IgM"
/tissue type="spleen"
/clone lib="genomic DNA in Charon 40"
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Manheimer-Lory, A., Katz, J.B., Pillinger, M., Ghoseein, C., Smith, A. and Diamond, B. Manond, B. Manond, B. Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype J. Exp. Med. 174 (6), 1639-1652 (1991) 92078875
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Insulin and igf-1 receptor agonists and antagonists
Patent: WQ 0172771-A 2352 04-0CT-2001;
DGI Fish-Technologies, L.L.C. (US); Novo Nordisk A/S (DK)
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//note="complementarity determining region, CDR 2"
265. _285
/note="complementarity determining region, CDR 3"
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llarity 100.0%; Pred. No. 1.8e-94;
Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="complementarity determining region,
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71. .102
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/trānslation="MRVPAQLLGLLLLWLPDTKCDIOMTQSPSSLSASVGNRVTITCR
ASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFSLTISSLQPED
VATYYCQKYNSVPRTFGQGTKVEIKRTVL"
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/tissue type="spleen"
/clone_lib="lambda zap II phage library"
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/protein_id="CAA51130.1"
/db_xref="GI:441393"
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/product="Ig kappa light chain (VJC)"
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Pred. No. 7.1e-86;
0; Mismatches 6
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                                                                 /organism="Homo sapiens"
/isolate="M.L."
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chromosome="2"
                              Location/Qualifiers
1. .395
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346. .384
/note="J-Kappa 1"
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97.28;
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/partial
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                                                                                                                                                                                                                                                            /translation="DIQMTOSPSSLSASVGDRVTITCRASQCISNVLAWYQQRPGKVP
KLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPPLFGGGT
KVEIKRIRARA"
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H.sapiens mRNA for rearranged Ig kappa light chain variable region
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Expressed human immunoglobulin kappa genes and their hypermutation
Eur. J. Immunol. 23 (12), 3248-3262 (1993)
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Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische
Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X72462.
X72462.1 GI:441392
C-region; immunoglobulin; J-segment; kappa light chain; V-region.
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 395)

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                                                                                                                                                                                                                                                                                                                                                                Length 338;
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                                                                                                                                                                                                              product="Ig kappa chain V-region"
protein id="AAB48616.1"
'db_xref="G1:1864137"
                                                                                                                                                                                                                                                                                                                                                             Score 300.4; DB 9;
Pred. No. 7.2e-86;
                                                                                                                                                                                                                                                                                                                81 t
                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
             /organism="Homo sapiens'
db xref="taxon:9606"
/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 GGAGGACCAÁGGTGGAGATCAAÁCG 323
                                                                                                                                                                                                                                                                                                              81 9
                                                                                                                                                          /gene="VL-COL"
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                                                                                                                                                                                              codon_start=1
                                                                                                              1. .338
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                                                                                                                                                                                                                                                                                                                                                              91.9%;
97.2%;
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                                                                                                                                              <1. .>338
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Best Local Similarity 97.2
Matches 317, Conservative
                                                                                                                                                                                                                                                                                                              92
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Homo sapiens
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AUTHORS
TITLE
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TITLE
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                                                                                                              gene
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Horocopiens IGK mRNA for immunoglobulin kappa light chain VLJ AB063945 I GI:21669096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 GCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 GCCGGGCGAGTCAGGGATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 TTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 TICCIAAGCICCIGAICIAIGCIGCAICCACTITGCAAICAGGGICCCAICTCGGITCA 187
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 447;
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.2%; Score 298.2; DB 9;
98.1%; Pred. No. 3.6e-85;
tive 0; Mismatches 3;
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/lissue_lib="BWHIV"
<1.5447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 t
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/note="G00-128-528"
119 c 108 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 CCAAGGTGGAAATCAAACG 326
                                                                                                                                                                                                                                               <ī. .>447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.1'
Matches 313; Conservative
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AB063945
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SVDTDNYARFWQGTLUTVASSGGGSGGGGGSGGSDIQMTQSPSSLSASVGDRVTIT
CRASQGTSNYLAWYQQKRGYPLFGGTKVPEIK"

201 c 219 g 162 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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1 (Dases I to 447)

Collet, T.A., Roben, P., O'Kennedy, R., Barbas, C.F. III, Burton, D.R. and Lerrer, R.A.

A binary plasmid system for shuffling combinatorial antibody libraries

Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
         Parent: WO 0172711-A 2344 04-0CT-2001;
DGI BioTechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 91.3%; Score 298.4; DB 6; Length 761; Best Local Similarity 97.2%; Pred. No. 3.1e-85; Matches 315; Conservative 0; Mismatches 6; Indels 3;

    447
    organism="Homo sapiens"

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L03152.1 GI:185387
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<1. .>328
/codon start=1
/codon start=1
/product="immunoglobulin light chain variable region"
/protein_id="AAR94864.1"
/protein_id="AAR94864.1"
/db xxef="id:18025710"
/translation="IQMTOgPSSLGASUGDRVTITCRASQGISNYLAWYQQKPGKVP
KLLIYAASTLQSGVPSRFSGGSGTDFTLTISSLQPEDVATYYCQKYNSAPRMYTFGQ
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Homo sapiens clone FD2K myosin-reactive immunoglobulin light chain variable region mRNA, partial cds.
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          Ghiotto, F., Fais, F., Valetto, A., Albesiano, E., Allen, S., Schluman, P., Vinciguerra, V., Rai, K., Ferratini, M. and Chiorazzi, N. Ig VL gene repertoire in B cell type chronic lymphocytic leukemia Unpublished
                                                                                         2. (bases 1 to 328)
Albasiano, E., Allen, S.,
Schulman, P., Vincipuerra, V., Rai, K., Ferrarini, M. and Chiorazzi, N.
Direct Submission
Submitted (29-470N-2001) North Shore-LIJ Research Institute, 350
Community Drive, Manhasset, NY 11030, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAAAGTTCCTAAGGTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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1 (bases 1 to 324)
Wu,X., Liu,B., Van der Merwe,P.L., Kalis,N.N., Berney,S.M. and Young,D.C.
                                                                                                                                                                                                                                                                                              /db xref="taxon:9606"
/ceIl type="B lymphocyte from patient with IgM+ chronic
lymphocytic leukemia (CLL)"
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/isolate="MCLL141"
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Matches 315; Conservative
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<1. ..324
/gene="IGK"
/codon_start=1
/product="immunoglobulin kappa light chain VLJ region"
/protonin_id="maxc01573.1"
/db_xref="G1:21669097"
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Homo sapiens MCLL141 immunoglobulin light chain variable region
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 328)

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XS Kurosawa,Y.

XS Kurosawa,Y.

Direct Submission

AL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujta Health University; Kutsukake-cho, Toyoake 470-1192, Japan

(E-mail:kurosawa@tujita-hu.ac.jp, Tel:81-562-93-9387)

Please visit our web site

URL:http://www.fujita-hu.ac.jp/immunity/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                /clone lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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Pred. No. 7.8e-85;
0; Mismatches 8;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="K118"
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Matches 315; Conservative
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LIYAASTLQPGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGQGTKV
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Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region
(IGIV@) mRNA, partial cds.
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1 (bases 1 to 450)
2 (Collet, T.A., Roben, P., O'Kennedy, R., Barbas, C.F. III, Burton, D.R. and Lerner, R.A.
A binary plasmid system for shuffling combinatorial antibody libraries
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Pred. No. 3.3e-84;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGGGACCAAGGTGGAAATCAAA 324
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                                                                                90.3%;
96.6%;
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                                                                            Query Match
Best Local Similarity 96.6<sup>,</sup>
Matches 313; Conservative
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ATYXCQKXNSAPYTFGGGTKLBIK"
a 195 c 221 g 174 t
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CRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGGGTDFTLTISSLQP
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Insulin and igf-1 receptor agonists and antagonists
Patent: WO 0172771-A 2394 04-0CT-2001,
DGI BioTechnologies, L.L.C. (US); Novo Nordisk A/S (DK)
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111 c 95 t
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                                                                                                                                                                                                                                                                                         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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Choi.1.4., Park.S.G., Chung,J.H., Kim,I.J. and Hong,H.J.
Direct Submission
Submitted (12-007-1999) Microbiology, College of Medicine, INJE
University, 633-165 Gaegum-Dong Jin-GU, Pusan 614-735, South Korea
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="Fab monoclonal antibody against preS1 of hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Metazoa, Chordata, Catarthini, Hominidae, Homo.

Mammalia, Eutheria, Primates, Catarthini, Hominidae, Homo.

I (baesa I to 316)

Choi, I. H., Park, S. G., Chung, J. H., Kim, I. J., and Hong, H. J. Generation of human Pab monoclonal antibodies against presl of Hoppinits B virus using repertoire cloning
                                                                                                                                                                                                                                      1 GAGCTCCAGATGACCCCAGTCTCCATCTGTTGTAGGAGACAGAGTCACC 60
                                                                                                                                                                                                                                                                                                                                                            241 GAAGATGTTGCGACTTATTACTGTCAAAAGTATGACAGTGCCCCTC---GCACTTTCGGC
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                                                                                                                                  Query Match

88.4%; Score 289.2; DB 9; Length 390;
Best Local Similarity 95.1%; Pred. No. 3e-82;
Matches 310; Conservative 0; Mismatches 13; Indels 3;
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AF193852
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1 (bases 1 to 390)
Chukwuocha, R.U., Hflao, B., Shaw, P., Witztum, J.L. and Chen, P.P.
Isolation, characterization and sequence analysis of five IgG monoclonal anti-phospholipid Pab fragments generated by phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="lymphocyte"
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VL-J-C region"
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Upublished
Upublished
Chukwuocha, R.U., Hflao, E., Shaw, P., Witztum, J.L. and Chen, P.P.
Direct Submission
Submitted (02-NOV-1998) Medicine/Rheumatology, UCLA, 32-59
Rehabilitation Center, 1000 Veteran Avenue, Los Angeles, CA
90095-1670, USA
                                                                                                                                                                            Gaps
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                                                                                                                                       Score 290.2; DB 9; Length 450;
Pred. No. 1.4e-82;
0; Mismatches 8; Indels 3
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/gene="IGHV@"
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Search completed: July 18, 2003, 13:47:34 Job time : 917.261 secs

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UI-HF-BLO UI-HF-BLO 602712592 AV733746 AGENCOURT UI-HF-BLO

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BG684416 826 bp mRNA linear EST 01-MAY-2001
602636169F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763993 5',
mRNA sequence.
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BG756818 602710291
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BQ707400 B
BG685552 6
AW405241 U
BG754732 6
AW406228 1
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AW383353
                                                            AW406562 BG540787 BQ706213 AW408194 BM818943 BG756519 BG684027
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BG341934 602463276
BG341941 602463283
BQ881840 AGENCOURT
BMS09065 1h16b08.x
AW404145 UI-HF-BL0
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      version.5.1.6
- 2003 Compugen Ltd.
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                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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BG341934
BG341941
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AW404145
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Copyright (c) 1993
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Result No.

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UI-HF-BLO

602715662 602635634 AGENCOURT AGENCOURT 602637525

Scoring table:

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Perfect score:

Sequence:

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Run on:

UI-HF-BLO K-EST0086 AGENCOURT

602245105 602144635 UI-HF-BLO

602713490

AGENCOURT 602498773

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/ clone="IMAGE:4576170"

/ clone="IMAGE:4576170"

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602463283F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576124 5',
mRNA sequence.
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Bakarycer, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria, Primates; Catarrhini; Hominidae; Homo.
Mammalla; Eutheria, Primates; Catarrhini; Hominidae; Homo.
Marional Libraria, Mago.nd..nih.gov,
National Institutes of Health, Mammallan Gene Collection (MGC)
National Institutes of Health, Mammallan Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue Procurement Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incryet Genemics. Inc.
Clone distribution: MGC clone distribution information can be
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/organism="Homo sapiens"
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/clone="Inba"NIH MGC_48"
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/lab host="bull0b (phage-resistant)
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/for average innert size 1.8kb . Library constructed by Ling
/Hong in the laboratory of Gerald Mr. Rubin (University of
/California, Berkeley) using ZAP-cDNA synthesis kit
/Stratagene) and Superscript II RT (Life Technologies).
/bottline is a NIH MGC Library."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 957)

S NIH-Mor http://mgc.nci.nih.gov/

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

Clone distribution: MGC clone distribution information can be thtp://image.llnl.gov

Plate: LLCM1288 row: g column: 19
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BG341934.1 GI:13148372
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Matches 311; Conservative
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/tissue_type="primary B-cells from tonsils (cell line)"
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Site_2: ECONI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhoI sites using the
following 5' adaptor: GGAGGAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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AGENCOURT_8642888 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6295725
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 888)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Pred. No. 1.8e-86;
0; Mismatches 5; Indels
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1288 row: e column: 21
High quality sequence stop: 616.
Location/Qualifiers
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Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
                                                                                                           organism="Homo sapiens"
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BQ881840
BQ881840.1 GI:22273848
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Best Local Similarity 97.5%;
Matches 318; Conservative
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate:.LLCMS502 row; g column: 22
High quality sequence stop: 655.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butterata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
In (bases It o. 358)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbaremail.nih.gow
Eco RI site shown at the beginning of the sequence.
Contact strauspergencion: M. B. Soares Lab
DNA Library Preparation: M. B. Soares Lab
DNA Sequencing by: M. B. Soares Lab
Clone distribution: MGC clone distribution information can be tound through the I. M.A.G. B. Consortium/LLNL at:
vww-bio.llnl.gow/bbrp/image/image.html
Seq primer: MI Strward.

1 contaction/Qualifiers
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935 bp 'mRNA linear EST 27-FEB-2001
62463029P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4575847 5',
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Pred. No. Se-79;
0; Mismatches 8; Indels 0;
                                                       IMAGE:3057865 5', mRNA
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AW404145.1 GI:6923202
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es 283; Conservative (
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Cher_ESTS: ihi6b08.y1

Conteact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Cher_ESTS: ihi6b08.y1

Endocrine Pancrass Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tal: 617-495-8557

Email admeltonobioth harvard.edu
Library was constructed by Dr. J. Perrer In vivo mass-excised to
University Genome Sequencing Center For information on obtaining a
plausecript SK. by Dr. H Inoue DNA Sequencing by: Mashington
Clone please contact: Dr. Hiroshi Inoue (hinoue@im.wistl.edu)
Sossible reversed clone: similarity on wrong strand
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Best Local Similarity 94.5%; Pred. No. 2.16-81;
Matches 308; Conservative 0; Mismatches 15; Indels 3; Gaps
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Matches 301; Conservative
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Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://amage.lln.gov
Plate: LLCM1287 row: j column: 08
High quality sequence stop: 673.
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                                                     Eukaryoja, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 935)
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                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AUTHORS
TITLE
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           Euteleostomi;
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Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: h column: 08
High quality sequence stop: 722.
Location/Qualifiers
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                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 773)
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92.3%; Pred. No. 9.9e-78;
iive 0; Mismatches 22
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/lab host="Organ: spleen; Vector: poTB7; Site_1: XhoI; Site_2: BcoRI, cDNA made by oligo-dr priming - Directionally cloned into EcoRI/XhoI sites using the following 5, adaptor: GGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                          Author sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

S Nil-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

Clone distribution. MGC clone distribution information can be http://image.llni.gov

Rubin. Government: Dr. Mark Blosciatorion information can be http://image.llni.gov

Rubin. Clone distribution. MGC clone distribution information can be http://image.llni.gov

Rubin. Library Requence stop: 651.

High quality sequence stop: 651.
  AGENCOURT 8475108 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301597
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Pred. No. 1.2e-76;
0; Mismatches 34; Indels
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                         57, mkwa sequence.
BQ707369
BQ707369.1 GI:21846268
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Local Similarity 89.6%;
Les 292; Conservative
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JOURNAL
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Home sapiens

Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Merazoa; Chordata; Catarrhini; Hominidae; Homo.

To the constitutes of Hall, Mammalian Gene Collection (MGC)

NIH-MGC Htp://mgc.nci.nih.gov/

NIE institutes of Hall, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Eco RI site shown at the beginning of the sequence.

CONA Library Preparation: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

CONA Library Preparation: MGC clone distribution information can be

NAN Sequencing by: MB. Soares Lab

CONA Library Preparation: MGC clone distribution information can be

clone distribution: MGC clone distribution information can be

now-bio.lln.gov/bbrp/image/image/image.html

Seq primer: M13 Forward:

Coration/Qualifiers

Location/Qualifiers

L AW405753

493 bp mRNA linear EST 16-FEB-2000
IMAGB: 3057290 5', mRNA sequence...
AW405753.1 GI:6924810 ή: 61 ATCACTTGCCGGGCGAGTCAGGGGCATTATTTTAGCCTGGTATCAGCAGAAACCA 120 180 240 251 311 241 GAAGATGTTGCAACTTATTACTGTCAAAGTATAACAGTGCCCCCTCCGAGTACGTTCGGC 300 312 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTC---GGACGTTCGGC 368 121 GGGAAAGTICÇTAAGCTCCTGATCTATGCTGCATTTTGCAATCAGGGGTCCCATCT 192 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 252 AGGTTCAGTGGCAGTGTGGGACAGATTTCACTCTCACCATCAGCAGCAGCT Gaps 3, Query Match 82.6%; Score 270; DB 10; Length 493; Best Local Similarity 91.4%; Pred. No. 2.7e-76; Matches 298; Conservative 0; Mismatches 25; Indels CAAGGGACCAAGGTGGAAATCAAACG 326 72 369 301 SOURCE ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE JOURNAL COMMENT BASE COUNT ORIGIN FEATURES

RESULT 11

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/clone liberories with MGC 48"
/tissue_type="primary B-cells from tonsils (cell line)"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab.host="DHIN MGC 48"
/lab.host="DHIN B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: BcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: agcAcCAGGG(G). Size-selected solobp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                      BG758398 921 bp mRNA linear EST 15-MAY-2001
602712592F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852678 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACATICCAGATGACCCAGTCTCCATCCTCCTGTCTGTAGGAGACAGAGTCACC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 ATCACTTGCCGGGCAAGTCAGAGCATTCGCAGCTATTTAAATTGGTATCAGCAGAAACCA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 GGGADAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                 Context: Robert Strausberg, Ph.D.

Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI697 row: h column: 23
High quality sequence stop: 848.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAACAGTCTGCAACCT
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                                                                                                                                                                                                                                                                                          1 (bases 1 to 921).

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Pred. No. 1.3e-75;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4852678"
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                                                                                                                                                   BG758398.1 GI:14069051
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89.0%;
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Best Local Similarity 89.0%
Matches 290; Conservative
                                                                                                          mRNA sequence.
BG758398
                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                         human.
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (15-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. Bento Soares, Ph.D."
                            AM407904
WI-HF-BLO-add-a-01-0-UI.x2 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061128 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (Dases 1 to 422)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                            Email: cgabbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Location/Qualifiers
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Site 1: EcoRV (destroyed); Site 2: Not!; RNA source pool
Of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT prined and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3:5 kb. Library is normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036: "
59 a 334 c 272 g 246 t 6 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1153)

8 NIH-MG http://mgc.nci.nih.gov/

8 National Institutes of Health, Mammalian Gene Collection (MGC)

1 (Dnyublished (1999)

8 Contact: Robert Strausberg, Ph.D.

8 Email: cgapbs-r@mail.nih.gov

7 Issue procurement: Invitrogen

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81.1%; Score 265.2; DB 13; Length 1153;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 422)
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118 c 117 g 99 t
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AUTHORS
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Gaps

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AW404992
UI-HF-BLO-abx-a-03-0-UI.rl NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3058060 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATCACTTGCCGGGCGAGTCAGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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                                                                                                                                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (baasa 1 to 391)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
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Copyright (c) 1993 - 2003 Compugen Ltd.
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327
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length DB II	DB	ID	Description
	304.8	93.2	743	24	ABK47275	Insulin/insulin-li
7	298.4			24	ABK47271	Insulin/insulin-li
n	295.2			24	ABK47272	Insulin/insulin-li
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Ŋ	295.2			24		Insulin/insulin-li
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7	278			24	ABK40186	Human/rabbit Ckapp
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o.	274.8			24		Human pancreatic t

HITT	Human anti-tu	UNA encoding the Human immunog	Humanised and											Human anti-Rh(D) c										702 Human endoglin (CD	ALIGNMENTS						receptor, DNA sequence #29.	tective, cerebroprotective, r; gene therapy, diabetes; 1; tumour, prostate; breast; diseases; stroke;							, Pillutla R, Brandt J; , Ostergaard S, Mandecki WS;
				21 AAA27381 24 ABQ54241																					ALIC		43 BP.	i o			th factor	Cytostatic; antidiabetic; neuroprote ophthalmological; insulin; receptor insulin-like growth factor-1; IGF-1 diabetic retinopathy; neurological diabetic neuropathy; gene; ss.	,			28.	28.	ES LLC.	Schaeffer L, J, Cheng W, Hsiao K;
				917																							DNA: 7		12	rst entry)	like growth	diabetic; ; insulin wth facto athy; neu				000WO-US0852	2000WO-US085	SIOTECHNOLOGIE NORDISK AS.	Blume AJ, Sc) Spetzler J, Ravera M, Hs
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                                                                                                                     The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are useful for treating diabetes. Also, peptides that are useful for treating insulin-like growth factor-1 (IGF-1) receptor are useful for treating insulin-like growth factor (IGF) sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. ABK47246-ABK47277 represent IR and/or IGF-1 receptor DNA sequences of the invention.
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                                     Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumours, comprises using peptides that bind to insulin or insulin-like growth factor receptors
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93.2%; Score 304.8; DB 24; Length 743;
Best Local Similarity 98.5%; Pred. No. 4.5e-87;
Matches 319; Conservative 0; Mismatches 2; Indels 3;
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                                                                                                Disclosure, Figure 39; 390pp; English.
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              WPI; 2002-025774/03.
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Mandecki WS;
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91.3%; Score 298.4; DB 24; Length 761;
Best Local Similarity 97.2%; Pred. No. 5e-85;
Matches 315; Conservative 0; Mismatches 6; Indels 3;
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Ostergaard S,
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J, Cheng
Hsiao K;
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                                                                                                               29-MAR-2000; 2000WO-US08528
                                                     29-MAR-2000; 2000WO-US08528
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Brissette R, Spetzler
Hansen PH, Ravera M,
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04-OCT-2001
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664 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTTTCACTTTCGGC 720 301 CAAGGAACAAAGTGAAA 324 301 CAAGGAACAAAGTGAAATCAAA 744	224, 7774 atandard; DNN; 722 SP. 224, 7774 atandard; DNN; 722 SP. 16-378-202 (first entry) 16-378-202 (first entry) 16-378-202 (first entry) 16-378-203 Specific and profit factor receptor, DNN sequence \$28. 16-378-203 Specific and profit factor receptor, DNN sequence \$28. 16-378-203 Specific and profit factor
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03	is Junkarov (first entry) Sequence #36. The properties of the proof factor receptor, DNA sequence #36. The proof of the proof factor is the properties of the proof of the
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Seguence 761 BP; 179 A; 200 C; 217 G; 165 T; 0 other;
    and/or IGF-1 receptor DNA sequences of the invention.
                                                       Score 295.2; DB 24
Pred. No. 5.2e-84;
                                                       Query Match 90.3%; Score 295.2; Best Local Similarity 96.6%; Pred. No. 5.2e Matches 313; Conservative .0; Mismatches
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96US-0599226.
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P-PSDB; AAW27568.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT88403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of modulating insulin activity in receptor (IR). A composition containing a peptide, optionally expressed agonist are useful for treating diabetes. Also, peptides that are antagonist are useful for treating diabetes. Also, peptides that are antagonists of the insulin-like growth factor-1 (IGF) receptor are useful for treating insulin-like growth factor (IGF)-sensitive tumours (e.g. & prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutiqs and research reagents. ABK47246-ABK47277 represent IR
544 GGGAAAGTICCTAAGCICCTGAICTAIGCTGCATCCACTITGCAATCAGGGGTCCCATCT 603
                                                                                                               604 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCAGCCT 663
                                                                                                                                                GGGAAAGTICCTAAAGCTCCTGAICTAIGCTGCAICCACTITGCAAICAGGGGTCCCAICT 180
                                                                                             181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumours, comprises using peptides that bind to insulin insulin-like growth factor receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pillutla R, Brandt J;
Ostergaard S, Mandecki WS;
                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insulin; receptor; gene therapy; diabetes; insulin-like growth factor-1; IGF-1; tumour; prostate; breast; diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                 Insulin/insulin-like growth factor receptor, DNA sequence #30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Figure 57; 390pp; English.
                                                                                                                                                                                                       CAAGGGACCAAGGTGGAAATCAAA 324
                                                                                                                                                                                                                         721 CAGGGACCAAGCTGGAGATCAAA 744
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Brissette R, Spetzler J, Cheng W,
Hansen PH, Ravera M, Hsiao K;
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                                                                                                                                                                                                                                                                                                  ABK47276 standard; DNA; 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                           61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
                                                                                                                                                                                                                                                                                                                                                          121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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light chain; variable region; inhibition;
treatment; sepsis, disease; autoimmune disease; infectious disease;
maligiancy; pulmonary disorder; intestinal disorder; hepatitis;
cardiac disorder; inflammatory bone disorder; repertusion injury;
bone resorption disease; coaqulation disturbance; burn; ELAM-1;
keloid formation; scar tissue formation; pyrexia; HUVEC;
periodortal disease; obestivy; radiation toxicity;
human umbilical vein endothelial cell; ds.
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DB 24; Length 761;
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Mankovich JA, McGuiness BT, Roberts AJ, Sakorafas P;
Salfeld JG, Schoenhaut D, Vaughan TJ, White M, Wilton AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA for anti-TNF-alpha antibody light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                     factor alpha (TNF-alpha) antibody (Ab) light chain variable region. The Ab dissociates from TNF-alpha with a Kd of LX10 power -8 M or less and has a Koff rate constant of LX10 power -3 s power -1 or less (both determined by surface plasmon resonance), and neutralises human TNF-alpha cytotoxicity in a standard in vitro L929 assay with an ICSO of LX10 power -7 M or less. The Ab, which inhibits TNF-alpha ctivity, can be used to treat sepsis, autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid spondylitis, osteoarthritis, gouty arthritis, allergy, multiple sclerosis, autoimmune diseases, malignancy, pulmonary, intestinal, cardiac or inflammatory bone disorders, bone resorption disease, alcoholic, viral or fulminant hepatitis, coadulation disease, alcoholic, viral or fulminant hepatitis, coadulation disease, alcoholic, viral or fulminant hepatitis, coadulation disease, alcoholic, viral or fulminant hepatitis, coadulation disease, alcoholic, viral or fulminant hepatitis, oscar tissue formation, pyrexia, periodontal disease, obesity and radiation toxicity. The Ab also inhibits TNF-alpha induced expression of endothelial call lelboyte adhesion molecule-1 (ELAM-1) on human umbilical vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 Arcacrigregegeaagreagegearcagaaarracriagecrigerarcageaaaacca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                     finity antibodies against human TNF alpha - useful to inhibit
ha activity, e.g. to treat autoimmune diseases and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody, Cgamma; Ckappa; Clambda2; ds; transgenic; vector; infectious disease; malignancy; cancer; tumour; autoimmune disease; humanised immunoglobulin; cytostatic; antibacterial; virucide; fungicide; light chain variable region; heavy chain variable region;
                                                                                                                                       anti-human tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 18; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 85.4%; Score 279.2; DB 18; Best Local Similarity 93.5%; Pred. No. 4.8e-79; Matches 303; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 321 BP; 85 A; 87 C; 74 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human/rabbit Ckappa chimaeric DNA sequence.
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                                                                                                                                       sequence encodes a novel
                                                                                          Disclosure; Page 75; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK40186 standard; DNA; 632 BP
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                   High affinity antibodies
TNF alpha activity, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endothelial cells (HUVEC)
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                High
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ABK40186
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transgenic animal, comprising a purtion of a human immunoglobulin pelates to a humanised immunoglobulin (Camma, Ckappa or Clambdal). Also included area 1) nucleic acid molecules comprising the clambdal). Also included area 1) nucleic acid molecules comprising the clambdal. Also included area 1) nucleic acid molecules comprising the clambdal. Also included area 1) nucleic acid molecules comprising the clambdal. Also included area 1) nucleic acid molecules comprising the clambdal. Also included area and read and read to replacing an Irg gene segment troom a non-human animal with a human immunoglobulin (Ig) gene segment from a non-human animal with a human immunoglobulin (Ig) gene segment, and a 3' nucleotide sequence, where the 5' and 3' nucleotide sequence, where the 5' and 3' nucleotide sequence, where the 5' and 3' nucleotide sequence, where the 5' and 3' nucleotide sequence of the igone segment from the non-human animal, 3) a transgenic vector comprising a human Ig gene segment is met a least one of the gene segments is a human ig gene segment segment is an unrearranged of a non-human animal, where the locus comprises multiple Ig gene segment segment and producing a repercoire of humanised by a useful for treating a disease caused by a partially or fully rearranged configuration, and the locus is capable of producing a functional repertoire of constant or variable region gene, or a chicken light chain constant or variable region gene, or a chicken light chain capable of producing the numanised antibodies, by introducing the construct into a recipient cell of a non-human animal and in the paraling the humanised antibodies, and transgenic construct into the genome of the recipient cell is a cell in an early embryo, or is a chicken and the recipient cell is a fertilised egg. Alternatively, transgenic construct into the genome of producing a functional repertoire of humanised hearth when animal degree of producing a functional repertoire of humanised hearth was in each the recipient cell is a fertilised egg. Alte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel humanised antibodies useful for treating diseases caused t
bacterial, viral, fungal infection and cancer, are derived from
transgenic non-human animals engineered to contain humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  humanised heavy or light chains, respectively are mated and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a humanised immunoglobulin derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 632 BP; 149 A; 169 C; 143 G; 171 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     Buelow J;
                                                                                                                                                                                                                                                                                                                                                                                                     Platzer J,
Chimeric - Oryctolagus cuniclus.
Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 11; 81pp; English.
                                                                                                                                                                                                            03-AUG-2000; 2000US-222872P.
15-MAR-2001; 2001US-276156P.
                                                                                                                                                                03-AUG-2001; 2001WO-US24348.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin loci
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-217188/27
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PLATZER J.
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                                                                  WO200212437-A2
                                                                                                              14-FEB-2002
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(BUEL/)
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2 ACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACCA 61

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Query Match 85.0%; Score 278; DB 24; Length 632; Best Local Similarity 92.9%; Pred. No. 1.5e-78; Matches 303; Conservative 0; Mismatches 20; Indels 3

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          301
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                                              GGTTCAGTGGCAGTGGATCTGGGACTGATTTCACTTACCATCAGCAGCCTGCAGCCTG
                                                                                                                                                                                     GGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTC
                                                                                                    GGAAGGITICCCAAGCTCCTGATTTATGCTGCATCCACTTTGCAATCTGGGGTCCCATCGC
                                                                                                                            GGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTG
                                 TCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy
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Thiaglingam A, Lewis ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, pancreatic tumour protein, pancreatic cancer, therapy, diagnosis, cancer, vaccine, cytostatic, ss.
corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides derived from pancreatic tumor cDNA library, useful as vaccines for preventing and treating pancreatic cancer, as well as for the diagnosis and monitoring of such cancers -
                                                                                                                                                                                                                                                                                                                                             104 GACATCCAGATGACCCAGTCTCCATCTTTCCTGTCTGCATCTGTAGAGACAGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
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                                                                                                                                                                                         DB 24; Length 565;
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                                                                                                                                                                                  Query Match 84.5%; Score 276.4; DB 24; Length Best Local Similarity 92.6%; Pred. No. 4.6e-78; Matches 302; Conservative 0; Mismatches 21; Indels
                                                                                                                              Sequence 565 BP; 128 A; 155 C; 142 G; 134 T; 6 other;
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21-SEP-2000; 2000US-234451P.
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relater to therapy and diagnosis of cancer, such as pancreatic cancer. The polypeptides and polymucleotides of the invention are useful as vaccines and pharmaceutical compositions for preventing and treating pancreatic cancer, as well as for the diagnosis and monitoring of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIGM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary; ds.
                                                                                                                                                                                                             GACATCCAGATGACCCCAGTCTCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACC
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                                                           cancers. The present sequence is human pancreatic tumour protein
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                                                                                                                                  DB 24; Length 737;
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                                                                                                                                                               32; Indels
                                                                                                     Sequence 737 BP; 188 A; 211 C; 181 G; 153 T; 4 other;
                                                                                                                                  Score 274.8; DB 2
Pred. No. 1.7e-77;
                                                                                                                                                               0; Mismatches
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                                                                                                                                  84.0%;
90.2%;
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                                                                                                                                                               294; Conservative
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                                                                                                                                                Local Similarity
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P-PSDB; ABB07183
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The invention provides a neuromodulatory agent (I) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS). (I) is capable of inducing remyelination, promoting cellular proliferation of glial cells, and promoting Ca2+ signaling with oligodendrocytes. An humanised antibody to (I) can be selected from antibody sHIGMSZ (LMW 22), ebvHigh Ms119B10, ebv High CG2B68, AKMF4, CB31B12, CB21E7 or MS119E5. (I) is useful for stimulating crawyelination of CNS axons, or treating demyelinating proliferation of glial cells in CNS axons, or treating demyelinating disease of CNS in a mammal in need of such therapy. (I) is preferably useful for treating a demyelinating disease of CNS. (I) is preferably useful for treating a demyelinating disease of CNS. (TMEV) or for treating a human being having multiple sclerosis, or a chuman or domestic animal with a viral demyelinating disease of CNS. (I) is also useful for simulating remyelination of CNS axons. The autibodies are useful for stimulating infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful for treating multiple sclerosis, parkinson's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating disease, CNS diseases, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents the CB2iE7 kappa light chain variable region nucleotide sequence.
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Novel neuromodulatory agent (a human IgM monoclonal antibody) promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis
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infection; inflammation, haematopoiesis; AIDS; allergy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1) Score 274.4; ilarity 97.9%; Pred. No. 1.66 Conservative 0; Mismatches
                                                                                                          42; 219pp; English
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Matches 278; Conserv
                                                                                                          Claim 43; Fig
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121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
                      67 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC
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127 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anticancer human monoclonal antibody variable region sequences - and related DNA and RNA
                                                                                                                                                                                                                                                                                                                              Human anti-tumour antigen antibody light chain variable region CDNA.
                                                                                                                                                                                                                                                                                                                                                                Human, tumour antigen, cancer, monoclonal, antibody, light chain, variable region; medicine; pharmacology; biochemistry; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human anti-tumour antigen monoclonal antibody (MAD) light chain variable region, useful medicine, pharmacology and biochemistry. The isotype of a MAD secreted by the human/human hybridoma HT was determined to be and kappa. Human MAD was purified, and the antigen recognised human MAD was purified, and the antigen recognised human MAD cLN*_ISM identified by western blocting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.6%; Score 270; DB 18; Length 396; Best Local Similarity 91.4%; Pred. No. 4.5e-76; Matches 298; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 396 BP; 101 A; 107 C; 97 G; 91 T; 0 other;
                                                                          CAAGGGACCAAGGTGGAAATCAAACG 326
                                                                                                           CAAGGGACACGACTGGAGATTAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 11; 14pp; Japanese.
                                                                                                                                                                                                                BP
                                                                                                                                                                                                                AAT75423 standard; cDNA; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95JP-0278266.
                                                                                                                                                                                                                                                                                          (first entry)
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/*tag=
67..396
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P-PSDB; AAW22842.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP09100300-A
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-1995;
                                                                                                                                                                                                                                                                                          12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
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                                                                                                                                                                                                                                                      AAT75423;
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                                                                                                                385
                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 GACATICCAGATGACCAGTCTCCATCCTCCTGTATCTGCATCTGTAGGACAGAGTCACC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the human immunoglobulin superfamily protein IGFAM.10 gene, which was isolated from a cDNA library of colon tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable fo diagnosing and treating many disease; including cancer, immune system arteriosclerosis, ashima, alberosclerosis, cholecystifis, croh's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriașis, iheumatoid arthritis, scleroderma, systemate, lupus arythematosus and ulcerative oolitis), complications of cancer, hammatogia and extracorporeal circulation, trauma and haematopoiețic cancer (such as leukaemia) and infections caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
181 CGGTTCAGTGGCAGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACATCCAGATGACCCCAGTCTCCATCCTCTGTTCTGTAGGAGACCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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B3.1%; Score 271.6; DB 21; Length 936;
Bert Local Similarity 89.6%; Pred. No. 1.96-76;
Matches 292; Conservative 0; Mismatches 34; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 936 BP; 239 A; 276 C; 214 G; 207 T; 0 other;
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Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacteria, viruses, fungi or parasites.
                                                                          /*tag= a
/product= "IGFAM-10"
19..84
/*tag= b
85.729
/*tag= c
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                                   Location/Qualifiers
19..732
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Corley NC,
Lal P, Hillman JL,
                                                                                                                                                                                                                                                                                                                                 99US-0113635.
98US-0113635.
99US-0128194.
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                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-387796/33.
P-PSDB; AAY96298.
                                                                                                                                                                                                                WO200029583-A2
                                                                                                                                                                                                                                                                                                                                 19-NOV-1998;
22-DEC-1998;
07-APR-1999;
  Homo sapiens
                                                                                                                                                                                                                                                                                             19-NOV-1999;
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                                                                                                                    sig_peptide
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GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTCAG---ACGTTCGGC 363
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                       247 AGGTTCAGTGGATGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                     GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                     Screening; functional polypeptide; ligand; non-functional; enrichment; single chain antibody; ScFv; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening for functional polypeptides which bind a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                 DNA encoding a single chain antibody (ScFv).
                                                                                                                                                            CAAGGGACCAAGGTGGAAATCAAACG 389
                                                                                                                                        CAAGGGACCAAGGTGGAAATCAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 67pp; English
                                                                                                                                                                                                                                                            AAX36070 standard; DNA; 720 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-GB03135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0066729
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97US-0065428
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                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomlinson I, Winter G;
                                                                                                                                                                                                                                                                                                                                                                                                   Screening; functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-288302/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9920749-A1
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397 GACATCCAGATGACCCAGTCTCCATCCTCCTGTTCTGTAGGAGACAGAGTCACC 456

1 GACATCCAGATGACCCAGTCTCCATCTCCTGCATCTGTAGGAGACAGAGTCACC

9

Gaps

3;

25; Indels

DB 20; Length 720;

82.6%; Score 270; DB 20; 91.4%; Pred. No. 5.6e-76;

0; Mismatches

Best Local Similarity 91.4 Matches 298; Conservative

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Query Match

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Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-althritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antimiertality; neuroprotective; antiatreriosolerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
                                                                    180
                                 516
                                                                                                     576
                                                                                                                                        240
                                                                                                                                                                           636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA
                                                                    GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
                                                                                                                                                          AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTCTGCAACCT
                                                                                                                                                                                                            241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC
                                                                                                                                                                                                                                           637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCT---AATACGTTCGGC
                                                                                                                                        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively i cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunoglobulin light chain kappa region subgroup type I DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tamaki I,
                                                                                                                                                                                                                                                                                                          CAAGGGACCAAGGTGGAAATCAAACG 719
                                                                                                                                                                                                                                                                                  CAAGGGACCAAGGTGGAAATCAAACG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 154; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           AAA11630 standard; DNA; 729
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98JP-0276882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SANY ) SANKYO CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-258930/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-1999;
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61
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AAA11630
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immunomodulatory, dermatological, immunosuppressive, thyromimetic, antinterutility, neuroprotective, antinifertility, neuroprotective, antinifertility, neuroprotective, antinifertility, neuroprotective, antinifertility, neuroprotective, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic disease sythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndcoern, Goodpasture syndrome, Crom's anemia, Addison's disease, thrombopenia purpura, insulin multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arreriosolerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively chinibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in mrine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents can human immunoslobulin light chain kappa variable region subgroup type I which is used in the construction of humanised anti-Fas antibody constructs described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGATTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTC---GAACGTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACATCCAGATGACCCCAGTCTCCATCCTCCTGTGTGTAGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 ATCACTTGCCGGCCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGGTCCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGTTCAGTGGCAGTGGAATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, mouse, humanised anti-Fas antibody; Fas/Fas ligand;
light Chain subunit, apoptosis; immunosuppressàve; antiallergic;
autoimmune disease; allergy; atopic; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 270; DB 21; Length 729;
Pred. No. 5.6e-76;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised anti-Fas antibody related PCR primer SEQ ID NO 76,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL46009 standard; DNA; 729 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.4%;
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTC---GAACGTTCGGC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAAAĞCCCCTAAĞCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 252
                                                                                                                                                                                                                                                             The invention relates to a preventive or treating agent for diseases caused by a bnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of induring appropriation a cell expressing Fas. The agent has immunosuppressive and antiallersy activity and is used for preventing and treating autoimmune pCR primer, useful to the invention.
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82.6%; Score 270; DB 24; Length 729;
Best Local Similarity 91.4%; Pred: No. 5.6e-76;
Matches 298; Conservative 0; Mismatches 25; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;
                                                                                                                                                                                                                          Example 15 (Preparatory); Page 40; 194pp; Japanese.
                                                                                                                                                                                      treating autoimmune diseases, allergy, and atopy
                                                                                                                                                                     containing humanised anti-Fas antibody,
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Job time : 86.7713 secs
                 28-MAR-2001; 2001JP-0093106.
                                                    29-MAR-2000; 2000JP-0090918.
                                                                                          (SANY ) SANKYO CO LTD.
                                                                                                                               WPI; 2002-145113/19.
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ptodata/1/pubpna/USO5_NEW_PUB.seq.2
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1439767 seqs, 1031500376 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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327
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2025, Ap	Sequence 186, App	Sequence 36, Appl	Sequence 37859, A	Sequence 7, Appli	Sequence 65, Appl		Sequence 1, Appli	٠.			101,	Sequence 112, App	Sequence 110, App	Sequence 210, App	3, Ap
SOMMAKIES	ID	2														US-09-848-798-210 Se	US-09-798-058-3
		15	15	12	12	11	15	10	11	15	15	11	12	12	12	12	10
	* Duery Watch Length DB	514	537	321	490	737	819	720	720	729	321	974	324	324	324	324	326
	% Query Match	89.9	89.9	85.4	85.0	84.0	84.0	82.6	82.6	82.6	81.0	9.08	80.6	90.6	80.1	80.1	79.6
	Score	294	294	279.2	278	274.8	274.8	270	270	270	264.8	263.6	263.4	263.4	261.8	261.8	260.4
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61 ATCACTTGCCGGGCGAGTCAGGCCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

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0007800111000111000	Sequence 3, Appli Sequence 3, Appli Sequence 98, Appli Sequence 107, App Sequence 32, Appl
US-09-878-178-1811 US-10-046-935-1811 US-10-165-3-1811 US-10-165-3-1811 US-10-167-3-1811 US-10-167-3-1811 US-10-167-3-181 US-10-167-181-18 US-10-167-181-13 US-10-167-181-13 US-10-167-181-13 US-10-1848-798-102 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-222 US-09-848-798-204 US-09-905-243-57 US-09-848-798-100	-10-060-585- -10-172-317- -09-848-798- -09-848-798-
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ALIGNMENTS

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GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTTGCATCTGTAGGAGACAGAGTCACC 137
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Pred. No. 8.2e-92;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                     THE THERAPY
                                                                                                                                                                                                                          APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Smith, Carcole L.
APPLICANT: Smith, Carcole L.
APPLICANT: Stolk, John A.
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.9%; Score 294; 96.0%; Pred. No. 8
                 Sequence 2025, Application US/10066543 Publication No. US20030087818A1 GENERAL INFORMATION:
                                                                                     APPLICANT: Jiang, Yuqiu
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                           Secrist, Heather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 89.9
Best Local Similarity 96.0
Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-066-543-2025
JS-10-066-543-2025
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                                                                                                                                                197 GAAGAIGITGCAACTIAITTCTGTCAAAAATATAACAGTGCC---CCCGGGACGTTCGGC
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85.4%; Score 279.2; DB 12; Length
Best Local Similarity 93.5%; Pred. No. 9.4e-97;
Matches 303; Conservative. 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ 1D NO: 36:
US-09-801-185A-36
                                                                                   140 CAAGGGACCAAGGTGGACATCAAACG 115
                                                            301 CAAGGGACCAAGGTGGAAATCAAACG 326
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                                                                                                                                                258 CGGTTCAGTGGCAGTGGGACACATTTCACTCTCACCACCATCGGCAGCCTGCAGCCT 317
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  ATCACTTGCCGGGCGAGTCAGGCCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 197
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                                                                          198 GGAAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCTGGGGTCCCATCT 257
                                                                                                                                                                                                                                      318 GAAGATGTTGCAACTTATTTCTGTCAAAATATAACAGTGCC---CCCGGGACGTTCGGC 374
                                                                                                                    CGGTTCAGTGGCAGTGTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                      US-10-066-543-186/C

Sequence 186, Application US/10066543

Publication No. US20030087818A1

GENERAL INFORMATION:

APPLICANT: Jiang' Yuqiu

APPLICANT: Jiang' Yuqiu

APPLICANT: Indirias Carol Yoseph

APPLICANT: Lodes, Michael J.

APPLICANT: Barger, Garter

APPLICANT: Samith, Heather

APPLICANT: Samith, Carle L.

APPLICANT: Smith, Carole L.

APPLICANT: Smith, Carole L.

APPLICANT: Smith, Sanger, Garter

APPLICANT: Scork, John Dardon

APPLICANT: Smith, Sanger, Garter

APPLICANT: Scork, John Dardon

APPLICANT: Scork, John Dardon

APPLICANT: Scork, John Dardon

APPLICANT: Smith, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, Sandth, S
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                                                                                                                                                                                                                                                                                CAAGGGACCAAGGTGGAAATCAAACG 326
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CCATION: 529
CTHER INFORMATION: n = A,T,C or G
US-10-066-543-186
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ORGANISM: Homo sapiens
  138
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84.0%; Score 274.8; DB 11; Length 737;
Best Local Similarity, 90.2%; Pred: No. 4.4e-85;
Matches 294; Conservative 0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.0%; Score 274.8; DB 15; Length 819; 92.3%; Pred. No. 4.6e-85; ive 0, Mismatches 22; Indels 3;
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER FILE REPERENCE: 210121.543
CURRENT APPLICATION WIDBER: US/09/919,344
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030073105A1 1329729.1
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Publication No. US20030073105A1

GENERAL INPORMATION:

APPLICANT: Lasek, Amy K.W.

APPLICANT: Sornasse, Thierry

TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER

FILE REFERENCE: PA-0030-1 US

CURRENT APPLICATION NUMBER: US/10/158,646

CURRENT FILING DATE: 2002-05-29

FRIOR APPLICATION NUMBER: 60/295,239

PRIOR APPLICATION NUMBER: 60/295,239

RAIOR FILING DATE: 2001-05-31

NUMBER OF SEQ ID NOS: 78

SEQ ID NO 65

LENGTH: 819
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                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature, LOCATION: 669, 685, 718, 722 COTHER INFORMATION: n = A,T,C' or G' US-09-919-344-7
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Best Local Similarity 92.3
Matches 301; Conservative
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTESEQ for Windows Version 3.0
SEQ ID NO 37859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | NAME/KEY: misc_feature
| LOCATION: (1)...(490)
| CTHER INFORMATION: n = A,T,C or G
US-09-918-995-37859
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Patent No. US20020137911A1
GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
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Matches 303; Conservative
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ORGANISM: Homo sapiens
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Query Match
B2.6%; Score 270; DB 11; Length 720;
Best Local Similarity 91.4%; Pred. No. 2e-83;
Matches 298; Conservative ), Mismatches 25; Indels
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; ORGANISM: Homo sapiens
US-09-968-561A-1
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                   86 GACATCCAGATGACCCAGTCTCCATCTTGCATCTGCATCTGTTGGAGACAAAGTCACC
                                                                                                                             206 GGGACAGCCCCTAACCTCCTGATCTATGGTGCTCTTTGCAATCAGCTGTCCTTTT
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GACATCCAGATGACCCAGTCTCCATCCTCCTGTGCATCTGTAGGAGACAGAGTCACC
                                                                                                            GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
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; Sequence 1. Application US/09192854
; Patent No. US2002068276A1
; GENERAL INFORMATION
; APPLICANT: Winter, Greg
; APPLICANT: Winter, Greg
; TILE REFERENCE: 3789/72916
; FILE REFERENCE: 3789/72916
; CURRENT FILING DATE: 1998-11-17
; EARLIER FILING DATE: 1998-11-17
; SOFTURER FILING DATE: 1997-11-21
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO: 212
; SEQ ID NO: 212
; SEQ ID NO: 212
; SEQ ID NO: 212
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CORGANISM: Homo sapiens
US-09-192-854-1
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Sequence 1, Application US/09968561A

Sequence 1, Application US/09968561A

Sequence 1, Application US/09968561A

Batel No. US20020164642A1

GENERAL INFORMATION:

APPLICANT: TOTALE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

FILE REFERENCE: 8039/1073B

CURRENT APPLICATION NUMBER: US/09/968,561A

PRIOR FILING DATE: 1997-10-20

PRIOR APPLICATION NUMBER: US 60/065,248

PRIOR PELING DATE: 1997-11-13

PRIOR PELING DATE: 1997-11-21

PRIOR PELING DATE: 1998-10-20

PRIOR PELING DATE: 1998-10-20

PRIOR SED ID NOS: 350

SOFTWARE: PatentIN Version 3.1

LENGTH: 720
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Sequence 125, Application US/10216484
Sequence 125, Application US/10216484
GREERAL INFORMATION:
GREERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Makahara, Kaori
APPLICANT: Takahara, Kaori
APPLICANT: Takahara, Cohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CAAGGGACCAAGGTGGAAATCAAACG 719
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240 300

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61 ATCACTTGTCGGGCGAGTCAGGGTATTAGCAGGTGGTTAGCCTGGTATCAGCAGAACCA 120
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                                                                                                                                                   61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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APPLICANT: TSUJ, Takashi
APPLICANT: TSUJ, Takashi
APPLICANT: TSUJ, Takashi
APPLICANT: HOTI, No. US2020102658Aluaki
APPLICANT: HOTI, No. US2020102658Aluaki
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFRENCE: 06501-07901
CURRENT APPLICATION NUMBER: US 09/859,053
CURRENT APPLICATION NUMBER: UP 2001-9508
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-05-18
                                                                                  1 GACATCCAGATGACCCAGTCTCCATCCTCATCTGCATCTGTAGGAGACAGAGTCACC
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            Gaps
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         27; Indels
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Pred. No. 3.8e-81
0; Mismatches 2
         Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 90.23
Matches 294; Conservative
         294; Conservative
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LOCATION: (39):..(104)
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Publication No. US20030031667A1

GENERAL INFORMATION:

APPLICANT: Boo. Yashwart M.

APPLICANT: Keler, Tibor

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC

CURRENT APPLICATION NUMBER: US/10/035,637

CURRENT FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2000-05-08

PRIOR FILING DATE: 2000-05-08

PRIOR FILING DATE: 2000-09-07
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Pred. No. 9.5e-82;
                                                                                                                                                                                                                                                                                                                  Length 729;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                  Score 270; DB 15; 1 Pred. No. 2e-83; 0; Mismatches 25;
            CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
LENGTH: 729
CURRENT APPLICATION NUMBER: US/10/216,484
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 321
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Best Local Similarity 91.4%;
Matches 298; Conservative
                                                                                                                                                                                                               TYPE: DNA
GORGANISM: Homo sapiens
US-10-216-484-125
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; LOCATION: (1)...(321)
US-10-035-637-1
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Best Local Similarity
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US-09-848-798-112

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RESULT 12
() 9-848-798-101
() Sequence 101, Application US/09848798
() Sequence 101, Application NO US20030040605A1
() Febblication NO US20030040605A1
() Publication NO US20030040605A1
() FILE REPERINCE SIGGE, Donald L.
() TITLE OF INVENTION: Rh(D) BINDING PROPUCTION THEREOF
() TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
() TITLE OF INVENTION: UNMBER: US/09/848,798
() CURRENT FILING DATE: 2001-05-04
() PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
() PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-11
() NUMBER OF SEQ ID NOS: 224
() SEQ ID NO 101
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121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
225 GGGAAAGCCCCTHAAAACTCCTGATCTATGTTTGCATCGATTTGCAAGTGGGGTCCCATCA 284
                                                                                                                                                                                                                                                                      241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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                                                                                                                                                                                                                                                                                                             345 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTC---CCGTGGACGTTCGGC 401
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80.6%; Score 263.4; DB 12; Length
Best Local Similarity 88.8%; Pred. No. 2.9e-81;
Matches 285; Conservative 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             301 CAAGGGACCAAGGTGGAAATCAAACG 326
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; OTHER INFORMATION: anti-Rh(D) chain 101
NS-09-848-798-101
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ORGANISM: Homo sapiens
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Sequence 112, Application US/09848798

FUDIcation No. UG20030040605A1

GRUERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE:

TORRENT PAPLICATION NUMBER: US/09/848,798'

CURRENT PAPLICATION NUMBER: US/09/848,798'

CURRENT PAPLICATION NUMBER: BALLIER APPLICATION NUMBER: 09/240,274

FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274

FRIOR PILING DATE: EARLIER FILING DATE: 1999-01-29

FRIOR PILING DATE: EARLIER FILING DATE: 1999-1128

FRIOR FILING DASE: EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SEQ ID NO 112

LENGTH: 324
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80.6%; Score 263.4; DB 12; Length 324;
Best Local Similarity 88.8%; Pred. No. 2.9e-81;
Matches 285; Conservative 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                              ), OTHER INFORMATION: anti-Rh(D) chain 112
US-09-848-798-112
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Sequence 210, Application US/09848798

Publication No. US2030040665A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Bh(D) - BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REPERBENCE: 05596-42U2

CURRENT FILING DATE: 2001-05-04

PRIOR FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274

PRIOR RILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 210

LENGTH 23.4
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US-09-848-798-210
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Pred. No. 1.1e-80;
                                                                                             Query Match 80.1%; Score 261.8; DB 1
Best Local Similarity 88.5%; Pred. No. 1.1e-80;
Matches 284; Conservative 0; Mismatches 37
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; ORGANISM: Homo sapiens
; FEATURE;
; OTHER INFORMATION: anti-Rh(D) chain I10
US-09-848-798-110
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Best Local Similarity 88.5
Matches 284; Conservative
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ORGANISM: Homo sapiens
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US-09-848-798-210
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123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCGGTTTGCAAAGTGGGGTCCCATCAAGGTT 182
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                                                246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG
                               186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA
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(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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327
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Description	Sequence 36, Appl	Sequence 101, Ay Sequence 112, Ay Sequence 110, Ay	210, 31, A	Sequence 33, Appl Sequence 3, Appli	220,	102,	Sequence 218, Ay Sequence 221, Ay		204,	Sequence 100, App.	206,	360,	. #	Sequence 4, Appli	98	107,	105,	Ċ
QI	US-09-125-098-36	US-09-240-274-101 US-09-240-274-112 US-09-240-274-110	US-09-240-274-210 US-08-378-939-31	US-08-378-939-33 US-09-343-485A-3	US-09-240-274-220 US-09-240-274-224	US-09-240-274-102	US-09-240-274-218 US-09-240-274-221	US-09-240-274-222	US-09-240-274-204	US-09-240-274-100	US-09-240-274-206	US-09-042-353-360	US-08-758-41/A-208 US-08-157-101A-8	US-08-157-101A-4	US-09-240-274-98	US-09-240-274-107	-60-	US-09-240-274-216
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253.8 253.8 252.2 252.2

257 256.8 255.4 255.4

28	251.4	76.9	388	4	US-09-042-353-358	Seguence		Api
29	251.4	76.9	388	4	US-08-758-417A-206			Apr
30	250.6	9.92	321	4	US-09-240-274-201	Seguence		App
31	249	76.1	321	4	US-09-240-274-205	Seguence	205,	Ap
32	249	76.1	321	4	US-09-240-274-211	Sequence		Apr
33	249	76.1	321	4	US-09-240-274-215	Seguence		Api
34	249	76.1	321	4	US-09-240-274-217	Sequence		App
35	248.8	76.1	321	7	US-08-378-939-13	Sequence	13,	App]
36	247.6	75.7	324	~	US-08-378-939-23	Sequence	23,	App]
37	247.4	75.7	321	4	US-09-240-274-109	Sequence		Api
38	247.4	75.7	321	4	US-09-240-274-113	Sequence		Apr
39	246.4	75.4	847	-	US-08-053-131-184	Sequence	184,	App
40	246.4	75.4	847	Н	US-08-096-762-184	Seguence		Apr
41	246.4	75.4	847	4	US-09-042-353-47	Seguence	47,	Appl
42	246.4	75.4	847	4	US-08-758-417A-312	Sequence	-	App
43	246	75.2	324	~	US-08-378-939-17	Seguence	17,	Appl
44	246	75.2	384	н	US-08-259-372A-13	Sequence	13,	Appl
45	246	75.2	384	-	US-08-468-671-13	Seguence	13,	Appl

BBBBBBBBBBBB

ALIGNMENTS

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APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
NIVBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MASSACHUSELES
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
FILING DATE: 08-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/POCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
                                                                           Salfeld, Jochen G.
Allen, Deborah J.
Hoogenboom, Hendricus R.J.M.
Kaymakcalan, Zehra
Labkovsky, Boris
Mankovich, John A.
MGGuinness, Brian T.
Roberts, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                     E: LAHIVE & COCKFIELD 60 State Street, suite 510
                 ; Sequence 36, Application US/08599226
; Patent No. 6090382
                                                                                                                                                                                                                                                                    Schoenhaut, David
Vaughan, Tristan J.
White, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617) 227-7400
                                                                                                                                                                                                                                                       Sakorafas, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)227-5941
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
US-08-599-226-36
                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                             APPLICANT
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Score 279.2 279.2

263.4 261.8 261.8 261.8 260.4 260.4 259.8 259.8

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Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: anti-Rh(D) chain 101
US-09-240-274-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 CAAGGGACCAAGGTGGAAATCAAA 324
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REFERENCE/DOCKET NUMBER: BB1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR BEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TYPE: TOPOLOGY: linear
NOLECULE TYPE: CDNA
US-09-125-098-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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241 GAAGATGTGCAACTTATTACTGTCAAAGGTATAACCGTC---CACCGTATACTTTGGC 297
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                                                                                                                                                               Gaps
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APPLICANT: Salfeld, Jochen G.
APPLICANT: Allen, Deborah J.
APPLICANT: Allen, Deborah J.
APPLICANT: Allen, Deborah J.
APPLICANT: Raymackcalan, Schra
APPLICANT: Kaymackcalan, Schra
APPLICANT: Labkovsky, Boris
APPLICANT: Roberts, Andrew J.
APPLICANT: Sakorafas, Paul
APPLICANT: Sakorafas, Paul
APPLICANT: Sakorafas, Paul
APPLICANT: Walden, Tristan J.
APPLICANT: Wince, Michael
APPLICANT: Wilcon, Michael
APPLICANT: Wilcon, Michael
APPLICANT: Wilcon, Michael
APPLICANT: Wilcon, Michael
APPLICANT: Wilcon, Andrew J.
APPLICANT: Wilcon, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakorafas, Sakor
                                                                                      Score 279.2; DB 3; Length 321;
Pred. No. 1e-81;
0; Mismatches 18; Indels 3.
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ZUDINITI 05A
ZUDIN 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: WARDICATION DATA:
APPLICATION NUMBER: US/09/125,098
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 CAGGGACCAAGGTGGAAATCAAA 321
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,226
FILING DATE:
NAME: DECONIA, GIULIO A.,
REGISTRAFION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36, Application US/09125098
Patent No. 6258562
                                                                             Ouery Match
Best Local Similarity 93.5%;
Matches 303; Conservative (
        US-08-599-226-36
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US-09-240-274-101

US-09-240-274-101

Sequence 101, Application US/09240274

Sequence 101, Application US/09240274

Patent No. 6555455

FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: FAREMATION: OF PRODUCTION THEREOF

CURRENT PAPLICATION NUMBER: 05/09/240, 274

CURRENT FILING DATE: 1998-04-129

FAREMATIER APPLICATION NUMBER: 60/081,380

FAREMATIER APPLICATION NUMBER: 60/081,380

FAREMATIER PLING DATE: 1998-04-01

SARIER APPLICATION NUMBER: 60/081,380

FAREMATIER PLING DATE: 1998-04-01

SARIER APPLICATION NUMBER: 60/088,550

FAREMATIER PLING DATE: 1998-04-0-11

NUMBER OF SEQ ID NOS: 224

SEQ ID NO 101

LENGTH: 324
                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                  61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
                                                                                                                                                                                                                                                                                                                                                                    180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297
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                                                                                                                     9
                                                         1 GACATCCAGATGACCCAGTCTCCATCCTCTGTCTGTAGGAGACAGAGTCACC
                                                                                                                     1 GACATCCAGATGACCCAGTCTCCATCCTCCTGCATCTGTAGGGGACAGAGTCACC
                                                                                                                                                                                                                                                                                                           121 GGGAAAGTICCIAAGCICCIGAICTAIGCIGCAICCACITIGCAAICAGGGGICCCAICI
                                                                                                                                                                                                                                                                                                                                                             121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 CCAGAIGACCCAGTCTCCATCCTCTGTTGCATCTGTAGGAGACAGAGTCACCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 80.6%; Score 263.4; DB 4; Length 324; Best Local Similarity 88.8%; Pred. No. 1.4e-76; Matches 285; Conservative 0; Mismatches 36; Indels 0;
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Sequence 110, Application US/09240274

Facent No. 6225455

GENERAL INFORMATION:
FAPPLICANT'S Siegel, Donald L.
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SOSTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SOSTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SOSTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SOSTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION NUMBER: 05/09/240,274
CURRENT APPLICATION NUMBER: 06/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10

NUMBER OF SEQ ID NOS: 224

SOSTWARE: Patentin Ver. 2.0

SEQ ID NOS: 224

SEQ ID NOS: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT PELICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,50
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-01-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 TIGCCGGGCGGAGTCAGGAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 CAGTGGCAGTGGATCTGGGACACATTTCACTCTCACCATCAGCAGTTGCAACCTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 irriigcaaciracracraficaacagagiracagiracccrccgrafagiriiggccaggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 CCAGATGACCCAGTCTCCATCCTCCTGTCTGTAGGAGACAGAGTCACCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AGTICCTAAGCICCIGATCTAIGCIGCATCCACTIIGCAATCAGGGGICCCAICICGGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 261.8; DB 4;
Pred. No. 4.7e-76;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I10
US-09-240-274-110
           303 GACCAAGCTGGAGATCAAACG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACCAAGGTGGAAATCAAACG 326
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Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.1%;
88.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 80.1
Best Local Similarity 88.5
Matches 284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-240-274-210
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Patent No. 625455

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFRENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER PILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 112

LENGTH 324
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3 CGAGCTCACCCAGTCTCCATCCTCCTATCTGCATCTGTAGGAGACAGAGTCACCATCAC 62
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                                                                                                                                                                  123 AGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT
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                                                                                                                                             AGTICCIAAGCICCIGAICIAIGCIGCAICCACITIGCAAICAGGGGGICCCAICICGGII
                                                                                                                                                                                                                                                                                                                                                                TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTACACTTTTGGCCAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-112
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61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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                                                                                                                                                                                                                                                                                            Length 324;
                                                                                                                                                                                                                                                                                   Query Match 79.6%; Score 260.4; DB 2; Length 32 Best Local Similarity 89.6%; Pred. No. 1.3e-75; Matches 292; Conservative 0; Mismatches 31; Indels
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STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
CITY: U.S.
COUNTRY: U.S.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN Release #1.0, Version #1.25
CLASSIFICATION NUMBER: US/08/378,939
FILING DATE: US 07/952640
FILING DATE: US 01.DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/08378939
Patent No. 5876961
GENERAL INFRATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEBMIS, ALAN PETER
TITLE OF INVENTION: PROUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 CAAGGGACCAAGGTGGAAATCAAACG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 GGAGGGACCAAGGTGGAGATCAAACG 323
           TELEFAX: (202) 783-6031
INPORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS:
LENGTH: 324 base pairs
TYPE: mucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                  MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRATURE:
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US-08-378-939-31
                                                                                                                                                                                                                NAME/KEY:
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US-08-378-939-33
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                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                     Query Match 80.1%; Score 261.8; DB 4; Length 324; Best Local Similarity 88.5%; Pred. No. 4.7e-76; Matches 284; Conservative 0; Mismatches 37; Indels 0
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US-08-378-331

J Sequence 31, Application US/08378939

Patent No. 596661

SEQUENCE INFORMATION:

APPLICANT: LEMIS, ALAN PETER

TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSED: ROTHWELL, FIGG, ERNST & KURZ

STRIE:

CITY: MASINGTON

CITY: MASINGTON

CITY: MASINGTON

COUNTRY: U.S.

COUNTRY: U.S.

COUNTRY: U.S.

COUNTRY: BADABLE FORM:

MEDIUM TYPE: Floppy disk

CONTYRR READABLE FORM:

MEDIUM TYPE: Floppy disk

CONTYRR READABLE FORM:

MEDIUM TYPE: Floppy disk

CONTYRR READABLE FORM:

MEDIUM TYPE: Floppy disk

CONTYRR PERCHIN PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

RIGH APPLICATION UNDBER: US/08/378,939

FILING DATE: US OT/952640

REFERENCE/DOCKET NUMBER: US OT/952640

REFERENCE/DOCKET NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
NUMBER OF SEQ ID NOS: 224

SEQ ID NO.210

LENGTH: 324

TYPE: DNA

ORGANISM: Homo sapiens

FATURE:
COTHER INFORMATION: anti-Rh(D) antibody clone SH34

US-09-240-274-210
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US-09-240-274-220
                                                  ; OTHER INFORM
US-09-343-485A-3
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SEQ ID NO 220
LENGTH: 324
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Fatent No. 641377
General INFORMATION:
APPLICANT: REFF. MITCHELL R.
APPLICANT: BARNETT, RICHARD S.
APPLICANT: MAINMAILAN CELLS VIA HOMOLOGOUS RECOMBINATION NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES ITILE OF INVENTION: WAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
FILE REFERENCE: 037003-027807
CURRENT FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR PELICATION NUMBER: 08/09/31,715
PRIOR APPLICATION NUMBER: 08/023,715
PRIOR PELICATION DATE: 1999-02-13
PRIOR FILING DATE: 1999-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GACATCCAGATGACCCAGTCTCCATCCTCCTGTTGCATCTGTAGGAGACAGAGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                              Length 324;
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79.6%; Score 260.4;
Best Local Similarity 89.6%; Pred. No. 1.36
Matches 292; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 ggaggaccaaggregagarcaaace 323
                                              1808-118
                                                                                            TELEFAX: (202) 783-6031
TELEFAX: (202) 783-6031
TELEFAX: SEQUENCE CHARACTERISTICS:
LENGTH: 324 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                          30,377
NAME TERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 18
TELECOMMICATION INFORMATION:
TELEPHONE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                            ANTI-SENSE: NO FEATURE:
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                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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US-08-378-939-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RAIGH BETONER AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT PAPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER PILING DATE: 1998-04-10
EARLIER PILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
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                                                                                                                                                                                                                                                                                 61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA
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Description of Artificial Sequence: Synthetic DNA referred to as "Mandy"
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                                                                                          DB 4;
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Pred. No. 5.1e-75;
0; Mismatches 39;
                                                                                                                                      32;
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US-09-240-274-220
                                                                                       Score 259.8; DB 4
Pred. No. 9.6e-75;
0; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7908 CAAGGGACCAAGGTGGAAATCAAACGT 7934
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Patent No. 6255455
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87.9%;
                                                                                     Query Match
Best Local Similarity 89.33
Matches 292; Conservative
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Best Local Similarity 87.9°
Matches 282; Conservative
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ORGANISM: Homo sapiens
OTHER INFORMATION: OTHER INFORMATION:
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TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL TITLE OF INVENTION SORTING METHOD FOR PRODUCTION THEREOF.

CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT PILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER PILING DATE: 1998-04-10
EARLIER PILING DATE: 1998-04-10
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTIN OF SEQ ID NOS: 224
SEQ ID NO 102
LENGTH: 321
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Sequence 218, Application US/09240274
Fatent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: SNETTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4212
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-01-29
EARLIER FILING DATE: 1998-01-10
EARLIER FILING DATE: 1998-01-10
SERVIER FILING DATE: 1996-10-11
SOFTWARE: PARE PRODUCTION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTING DATE: 1996-10-11
SOFTWARE: PATENTING DATE: 3096-30-11
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH49
                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102
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US-09-240-224
Sequence 224, Application US/09240274
Fatent No. 6255455
Fatent No. 6255455
FARENT NO. 6255455
FARENT NO. 6255455
FILE REPERENCE: 69596-4202
FILE REFERENCE: 09596-4202
FURRENT FILING DATE: 1999-01-29
FARLIER APPLICATION NUMBER: 05/09/240,274
FARLIER APPLICATION NUMBER: 05/091380
FARLIER FILING DATE: 1998-01-29
FARLIER APPLICATION NUMBER: 60/081,380
FARLIER FILING DATE: 1998-01-0
FARLIER FILING DATE: 1998-01-0
FARLIER FILING DATE: 1998-01-0
FARLIER FILING DATE: 1996-10-11
FARLIER FILING DATE: 1996-10-11
FARLIER FILING DATE: 1996-10-11
FARLIER FILING DATE: 1996-10-11
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FARLIER FILING DATE: 1996-10-11
                                               CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGGAGGA 245
           AGCCCCTAAGCTCCTAATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTT 182
                                                                        TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
                                                                                                                                               TTGCCGGGCGAGTCAGGGAATTATTTAGCCTGGTATCAGGAAAGCAAGAAA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens ORGANISM: PEATURE: CTHER INFORMATION: anti-Rh(D) antibody clone SH56 US-09-240-274-224
                                                                                                                                                                                             306 GACCAAGGTGGAAATCAAACG 326
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18-08-240-274-102
'Sequence 102, Application US/09240274
'Patent No. 6255455
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Search completed: July 18, 2003, 19:59:06
Job time: 18.3396 secs
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SEQ ID NO 222
LENGTH: 321
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FACENCE NO. 0.273455

FITLE NOTE SIGGEL, Donald L.

FITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-4202

FILE REFERENCE: 09596-4202

FILE REFING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE PACENCY OF SEQ ID NOS: 224

SEQ ID NO 221

LENGTH: 321
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                                                                                                                                                                                       TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA
                                                                                                               6 CCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC
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                                         Length 321;
                                                                              Indels
                                                                              30;
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US-09-240-274-221
                                       Score 257; DB 4;
Pred. No. 1.7e-74;
0; Mismatches 30
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; Sequence 221, Application US/09240274
; Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACCAAGGTGGAAATCAAACG 326
                                         78.6%;
89.7%;
                                     Query Match
Best Local Similarity 89.7
Matches 288; Conservative
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US-09-240-274-218
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RA(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-01-29
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

HSVK4H2FG

ВВ

Match Length

Score

Query

Result

E01736 E01735

X70465 H. sapiens D E01736 Genomic DNA E01737 Genomic DNA U86791 Human Ig li L11700 Human immun Z18328 H. sapiens m AR058974 Sequence AR08878 Sequence

HUMIGLODR

E01737 HSU86791

S50732 immunoglobu BC017870 Homo sapi AF455557 Homo sapi X83714 H.sapiens m AB064111 Homo sapi

BC017870 AF455557

321.4 319.8 319.8 319.8

319

HUMIGKAW

AR088798

E05868 DNA sequenc M29467 Human Ig re S50732 immunoglobu

A29532 FLAG sequen A29530 Hum4 VL-CC4 AR09655 Sequence A29534 pSC49FLAG s AY043136 Homo sapi

112019 Sequence 3 AX300034 Sequence AF099194 Homo sapi AB063957 Homo sapi AB064075 Homo sapi

AB063957 AB064080 AB064075 A29532

A29530 AR096955 A29534 AY043136 A62121 AX022345

1330 1330 1359

A62121 Sequence 15 AX022345 Sequence 246347 H. Sapiens m AR096963 Sequence X02990 Human mRNA

HSBUD114L AR096963

HSVKIVR BC018761

E37603

X72457 H.sapiens m Z18329 H.sapiens m AX355947 Sequence

HSIGKLV36 HSIGKVBE AX355947 HUMIGLVBC

BC018761 Homo sapi

E37603 Monoclonal

L26536 Homo sapien E05213 cDNA sequen

AR096964 Sequence AF099195 Homo sapi S71450 Ig Vkappa=i

AR096964 AF099195 AF103492

309.2 308.6 308.6

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X02484 Human aberr AF103492 Homo sapi

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July 18, 2003, 04:46:48; Search time 948.849 Seconds (without alignments) 10397.705 Million cell updates/sec
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Homo sapiens. Homo sapiens Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 339) X70465.1 GI:38442 anti-DNA antibody; complementarity determining region; Ig kappa light chain; Ig light chain; Ig variable region; IgG; immunoglobulin; systemic lupus erythematosus. ORGANISM REFERENCE VERSION KEYWORDS SOURCE

is the number of results predicted by chance to have a

No.

Pred.

PRI 17-FEB-1993

HSVK4H2FG 339 bp DNA linear PRI 1 H.sapiens DNA for anti-DNA antibody light chain variable region, subgroup V(k)4 (H2F 1gG line).

DEFINITION RESULT 1 HSVK4H2FG LOCUS

ACCESSION

ALIGNMENTS

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Nakatani,T., Nomura,N., Horigome,K. and Noguchi,H. Human Arribody, Anvingody Gene And Corresponding Recombinant Patent: JP 1988267295-5 64-NOV-1988; SUMITOWO CHEM CO LID, SUMITOWO PHARMACEUT CO LID
Manheimer-Lory, A., Katz, J.B., Pillinger, M., Ghossein, C., Smith, A. and Diamond, B. Manond, B. Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype J. Exp. Med. 174 (6), 1639-1652 (1991) 92078875 1660528
                                                                                                                                                                                       Location/Qualifiers

1. 339

/organism="Homo sapiens"
/isolate="patient HER(SLE)"
/db Aref="tanen:9606"
/db Aref="tanen:9606"
/db Aref="Experimentation of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of the continuous of t
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/note="complementarity determining region, CDR 3"
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100.0%; Score 339; DB 9; Length 3:
Bet Local Similarity 100.0%; Pered. No. 3.3e-100;
Matches 339; Conservative 0; Mismatches 0;
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Homo sapiens.
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Homo sapiens.
Homo sapiens.
Homo sapiens.
Homo sapiens.
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.
No fases I to 619)
Nakatani, T., Nomura, N., Horigome, K. and Noguchi, H.
HUMAN ANTIBODY, ANTIBODY GENE AND CORRESPONDING RECOMBINANT
Batent: JP 1988267295-4 4 04-NOV-1988;
SUMITOMO CHEM CO LID, SUMITOMO PHARMACEUT CO LID
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/db_xref="taxon:9606"
_110 c 100 g 97
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HSU86791
Human Ig light chain gene variable domain (CLL-L1B) mRNA, partial
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Pritsch,O., Troussard,X., Davi,F., Macro,M., Dumas,G., Magnac,C., Clerget,F., Schroeder,H.W., Leporrier,M. and Dighiero,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT
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       HUMAN ANTIBODY, ANTIBODY GENE AND CORRESPONDING RECOMBINANT PATENT: JP 1988267295-A 6 04-NOV-1988; SUMITOMO CHEM CO LID, SUMITOMO PHARMACEUT CO LID
                                                                                                          26-NOV-1987 JP 1987298513
03-DEC-1986 JP 86P 288340
NAKATANI TOMOSUKE, NOMUKA NORIKO, HORIGOME KAZUHIKO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 341;
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Pred. No. 5.4e-96;
0; Mismatches 8;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
96 c 83 g 76
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                                                                                                                                                                                                                               strandedness: Double;
topology: Linear;
hypothetical: No;
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                                                                       JP 1988267295-A/6
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PD 04-NOV-1988
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PR 03-DEC-1986
NOGUCHI HIROSHI
PC C12R21.19),
PC C12R21.19),
PC C12R21.19),
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341 bp DNA linear PAT 29-SEP-1997
denomic DNA encoding V region of L-chain of monoclonal antibody
against pseudomonas aeruginosa exotoxin.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NAKATANI TOMOSUKE, NOMURA NORIKO, HORIGOME KAZUHIKO,
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/product='signal peptide of V region
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/db_xref="taxon:9606"
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(C12P21/02,C12R1:91);
strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
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L11700

V-region; complementarity determining region; immunoglobulin light chain; monoclonal antibody.

Homo sapiens CDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                  /product="ig light chain variable domain"
/protein id="AAB48604.1"
/bx rref="G1:1864112"
/translation="IQMTQSPDSIAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQ
KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQABDVAVXYCQQYYSTPW
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Pritsch,O., Troussard,X., Davi,F., Macro,M., Dumas,G., Magn
Clerget,F., Schroeder,H.W., Leporrier,M. and Dighiero,G.
Direct Submission
Submitted (24-JAN-1997) Unite d'Immunohematologie et
d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux,
75724
Restricted VH clan usage by siblings affected with Chronic Lymphocytic Leukemia
Unpublished
                                                                                                                                                                                                                         /map="2p11-2"
/cell type="B cells"
/note="patient with Chronic Lymphocytic Leukemia"
1. 355
/gene="CLL-L1B"
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96.2%; Score 326.2; DB 9; Length 355;
Best Local Similarity 97.6%; Pred. Nov. 5.4e-96;
Matches 331; Conservative 0; Mismatches 8; Indels 0
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/db_xxref="taxon:9606"
/chromosome="2"
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/gene="CLL-L1B"
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1 (Dases 1 to 339)
Mariette,X., Tsapis,A and Brouet,J.C.
Nucleotidic Sequence Analysis Of The Variable Domains Of Four Human Monoclonal IgM With An Antibody Activity To Myelin-Associated Unpublished
2 (Dases 1 to 339)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 372) Hoon, D.S., Wang, Y., Sze, L., Kanda, H., Watanabe, T., Morrison, S.L., Morton, D.L. and Irie, R.F. Molecular cloning of a human monoclonal antibody reactive to ganglioside GM3 antigen on human cancers GCCCCC Cancer Res. 53 (21), 5244-5250 (1993)
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/Organisme="Homo sapiens"
/db xref="taxon:9606"
/cell_line="L612 EBV transformed B-cell"
/cell_type="B-lymphocyte"
/tissue_type="blood"
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                                                     GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
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Hosokawa, S., Tagawa, T., Hirakawa, Y., Ito, N. and Nagaike, K.
Human monoclonal antibody specifically binding to surface of cancer 590287-A 4 23-NOV-1999;
Location/Qualifiers
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Pred. No. 2e-94;
0; Mismatches 11; Indels 0
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Sequence 4 from patent US 5990287.
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Matches 328; Conservative
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Mariette,X.
Direct Submission
Submitted (29-OCT-1902) Xavier Mariette, Laboratoire d'
Submitted (29-OCT-1902) Xavier Mariette, Laboratoire d'
Immunopathologie, Hopital, Saint-Louis, 1, avenue Claude Vellefaux,
Paris, 75010, France
Locaion/Qualifiers
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Human monoclonal antibody specifically binding to surface antigen
of cancer cell membrane
Patent: US 5837845-A 4 17-NOV-1998;
Location/Qualifiers
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/db xref="taxon:9606"
/ceIl_line="Epstein-Barr transformed lymphoblastoid
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Sequence 4 from patent US 5837845.
AR058974
AR058974.1 GI:5984551
                                                                                                                                                                     /tissue_type="blood"
1. 339
/product="kappa chain"
/note="VK IV family"
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Synthetic construct

attificial sequences.

1 (bases 1 to 342)

HOSOkawa, S., Tagawa, T., Hirakawa, Y., Ito, N. and Nagaike, K.

HOSOkawa, S. Tagawa, T., Hirakawa, Y., Ito, N. and Nagaike, K.

HOSOKawa, S. PE NONOCIONAL ANTIBODY AND GENE CODING THE SAME, HYBRIDOMA

AND ANTITUMOR AGENT

NATIONAL AND ANTITUMOR AGENT

NATIONAL ASEL CORP

PR 1993304987-A4

PP 1993304987-A7

PP 22-JUN-1992 JP 1992162849

PR 28-JUN-1992 JP 199 1P 158859, 28-JUN-1991 JP 91P 158860, PR
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                                                                                                                                                                    Unknown.
Unclassitied.
1 (bases 1 to 342)
Hosokawa, S., Tagawa, T., Hirakawa, Y., Ito, N. and Nagaike, K. Hosokawa, S., Tagawa, T., Hirakawa, Y., Ito, N. and Nagaike, K. Human monoclonal antibody specifically binding to surface of cancer cell membrane
Cancer cell membrane
Patent: US 5990297-A 4 23-NOV-1999;
Location/Qualifiers
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CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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                                                                                DNA
                                                                       342 bp
Sequence 4 from patent US 5990297.
AR088878
AR088878.1 GI:10015639
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                                                                                                                                                                                                                                                                                                                 /organism="unknown"
92 c 87 g
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JP 1993304987-A/4.
Unidentified.
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405 bp mRNA linear PRI 04-JAN-1995
Human Ig rearranged kappa-chain mRNA V-J1-region, hybridoma AE6-5,
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J-region; V-region; immunoglobulin-kappa; processed gene; variable
region subgroup VK.IV.
Human (patient POP) hybridoma AE6-5 DNA, clone pHuUCVK, derived
Homo sapiens
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Spatz,L.A., Wong,K.K., Williams,M., Desai,R., Golier,J., Berman,J.E., Alf.F.W. and Latov,M.
Cloning and sequence analysis of the VH and VL regions of an anti-myelin/DNA antibody from a patient with peripheral neuropathy and chronic lymphocytic leukemia decrement with peripheral neuropathy Immunol. 144 (7), 2821-2828 (1990)
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28-JUN-1991 JP 91P 158861
PI HOSOKAWA SETIKO, TAGAWA TOSHIAKI, HIRAKAWA YOKO, ITO NORIHIKO, PI HOSOKAWA SETIKO, TAGAWA TOSHIAKI, HIRAKAWA YOKO, ITO NORIHIKO, PI NAGAIKE KAZUHIRO
PC (12P21/08,A61K39/395,C12N5/28,C12N15/13//A61B10/00,C12N15/08,QPC (212P21/08,C12R1:91);
PC (12P21/08,C12R1:91);
CC strandedness: Single;
CC strandedness: Single;
CC topology: Linear;
CC topology: Linear;
CC topology: Linear;
CC Location/Qualifiers
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Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
a 92 c 87 g 75 t
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/translation="MVLQTQVFISLLIMISGAYGDIVMTQSPDSLAVSLGERATINCK
SQSSLLXSSNNKNYLAWYQQKRGQPPKLLIYMASTREGGVPDRFSGSGSGTDFTLTIS
SLQAEDVAVYYCQOYSTPPMRGGGTKVEIKRTVAAFSV"
124 c 120 g 100 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg,R.
Direct Submission
Submitted (03-DEC-2001) National Institutes of Health, Mammalian
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                                                    ry of Medicine created thi
original journal article.
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/product=1immunoglobulin M light chain V region"
/protein id="AAB24404.1"
/db_xref="G1:261240"
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                                                                                                                                                                                                  /gene="immunoglobulin M light chain V region"
18 .460
'Partial
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Pred. No. 2.1e-94;
0; Mismatches 11; Indels 0;
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                                                                                                                                                                                                                                                                      /gene="immunoglobulin M light
/note="anti-lipid A antibody;
                                                  GenBank staff at the National Library entry [NCBI glibbq 120606] from the or This sequence comes from Fig. 3A. Location/Qualifiers
                                                                                                                        1. .460
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .460
/partial
 Hybridoma 11 (5), 667-675 (1992)
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96.8%;
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SSQSLLYSSNNKNYLAWYQQREGQPPKLLIYWASTRESGVPDRFSGSGTDFTLTIS
SLQAEDVAVYYCQQYYSTPPMFGQGTKVEIKRT"
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1 (Dases 1 to 460)

Dorai, H., Bubbers, J.E. and Gillies, S.D.

Cloning and reexpression of a functional human IgM anti-lipid A antibody
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                                                                                                                      /gene="IGKV"
/note="Ig kappa-chain V-J1-region precursor"
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                                                                                                                                                                                                                                                                                                /gene="IGKV"
/note="Ig kappa-chain signal peptide"
61. .>405
/gene="IGKV"
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Homo sapiens
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/db_xref="GI:185921"
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/db_xref="taxon:9606"
/map="2p12"
1. .405
/gene="IGKV"
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369. .370
/gene="IGKV"
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completed: July 18, 2003, 13:47:35
He : 949.849 secs
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Matches 327; Conservative (
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Homo sapiens
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                                       WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapber.emaal.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
CONTECT: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M.; Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MVLQTQVFISLLMISGAYGDIVMTQSPDSLAVSLGERATINCK
SSQSVLYSSNNKNYFSWYQQKPGRPPKLLIYWASTREGVPDRFSGSGSGTDFTLTIS
SLQABDVAYVYCQQYYSTPOPTGQGTKVEIKRTVAAPPVFIFPPSDEQLKSGTDSTLTIS
LLNNFYPREAKVQMYKDNALOSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHVYY
ACEVTHQGLSSPVTKSFNRGEC"
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                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 35 Row: i Column: If the Clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.

1. 979
  Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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    753
    /codon start=1
    /product="similar to immunoglobulin kappa constant" (protect="ark17870.1"
    /db_xref="GI:17389702"

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94.8%; Score 321.4; DB 9; Length 979;
Best Local Similarity 96.8%; Pred. No. 2.3e-94;
Matches 328; Conservative 0; Mismatches 11; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db xref="Laxon:9606"
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/clone_lib="NIH_MGC_83"
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AF455557 342 bp mRNA linear PRI 09-JAN-2002
Homo sapiens clone RIZMVL6 anti-cardiolipin immunoglobulin light
chain mRNA, partial cds.
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by,P., Soley,A., Cerutti,M., Freyssinet,J.M., Pasquali,J.L. and
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (05-DEC-2001) Laboratoire d'immunopathologie, Institut
d'Immunologie et d'Hematologie, i place de l'Hopital, Strasbourg
67091, France
                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostor
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
( bases 1 to 342)
Lieby, P., Soley, A., Cerutti, M., Freyssinet, J.M., Pasquali, J.L.
Martin, T.
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Pred. No. 6.9e-94;
0; Mismatches 12;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                 Chordata;
Primates;
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/clone="RIZMVL6"
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Perfect score:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I. (Dassas 1 to 964)

I. (Dayblished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1694 row: h column: 18

High quality sequence stop: 784.
                                                                                                                                         BF128829 601811013
BG686522 602637474
BG766188 602144832
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BQ083970 K EST0105
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BQ082708 F
BM821681 F
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AW406512
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BQ082810
BM768906
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AW405821 UL-HF-BL0
AW402126 ILS-UM007
BG398034 602439564
AW390292 CM2-ST018
                                                                              July 18, 2003, 04:16:54; Search time 587.455 Seconds (without alignments) 9345.860 Million cell updates/sec
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                                                                                                                                                         1 gacatccagttgacccagtc......ggaccaaggtggaaatcaaa 339
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Compugen Ltd
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            GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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Score

Result No.

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321.4 319.8 318.2 311.8

RC1-HT025 K-EST0144

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AW405821 641 bp mRNA linear EST 16-FEB-2000 UI-HF-BLO-abp-h-07-0-UI.rl NIH MGC_37 Homo sapiens cDNA clone IMAGE:3057636 5', mRNA sequence.
AW405821 GI:6924878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 641)

NH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strauberg, Ph.D.

Email: Capubs-romail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDA Library Preparation: M.B. Soares Lab

CDN Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 GACATCGTGATGACCCAGTCTCCAGATTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
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    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases I to 886)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: capabs-remail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.AG.E. Consortium (LIML)

NNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:

Plate: LLCM1091 row: p column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               886 bp mRNA linear EST 21-DEC-2000 mRNA sequence.
BF674779
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Matches 326; Conservative
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Constructed from size fractionated cytoplasmic mRNA
Constructed from size fractionated cytoplasmic mRNA
M. Staudt, Ph.D. Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.

1 (bases 1 to 53)

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1 (brish M. A., de Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW802126 533 bp mRNA linear EST 16-MAY-2000 ILS-UM0071-120400-065-d06 UM0071 Homo sapiens cDNA, mRNA sequence.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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20202663
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                                                                                                                                                                                              B cells"
                                                                                                                                                                                                                                                                                                                                                                                      Score 319.8; DB 10;
Pred. No. 5.9e-87;
                                                                                                                       db_xref="taxon:9606"
clone="ImAce:3057636"
clone lib="NIH MGC 37"
tissue type="1ymph"
cell type="germinal center B
cell line="MGC8"
lab_Fost="DH10B (LTI)"
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                            /organism="Homo sapiens"
                                                                          Location/Qualifiers
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al Similarity 96.5%;
327; Conservative
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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MEDLINE
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/organism="Homo sapiens"

/db xref="taxon:9606"

/clone_lib="un0071"

/dev stage="Adult"

/note="Organ: uterus; Vector: puc18; Site_l: Smal; Site_2:
Smal; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
31 a 145 c 137 g 120 t
                                                                                                                                          Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpsoneJudwig.org.br

Email: saimpsoneJudwig.org.br

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/ecripts/gethtml2.pl?tl=&t2=IL5-UM0071-120

400-065-406cst3=2000-04-12&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 419.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                           Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTACCAGCAGAAAACCAGGACAGCCTCCTAAGCTGCTCTTTACTGGGCATCTACCCGG
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Indels
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// Organism="Mono sapiens"
// Organism="Mono sapiens"
// Clone lib="sznon:9606"
// Clone lib="sznon:9606"
// dev_ersge="Addit"
// note="Organ: stoneach; Vector: puc18; Site 1: Smal;
// note="Organ: stoneach; Vector: puc18; Site 1: Smal;
// note="Organ: stoneach; Vector: puc18; Site 1: Smal;
// note="Organ: stoneach; Vector: puc18; Site 1: Smal;
// note="Organ: stoneach; A minilibrary was made by cIoning products
derived from ORESTES PCR (U.S. Letters: Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc18 wector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions "
173 c 162 g 146 t
                                                                                                                                                                        Contracts Simpson A.J.G.
Contract: Simpson A.J.G.
Laborstroxy of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
Brazil
Tel: +55-11-2707001
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Fax: +55-11-2707001
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91.5%; Score 310.2; DB 10; Length
Best Local Similarity 94.7%; Pred. No. 5.1e-84;
Matches 321; Conservative 0; Mismatches 18; Indels
                                                             1 (bases 1 to 643)
HGGP http://www.ludwig.org.br/ORESTES.
The FAPESF/LICR Human Cancer Genome Project Unpublished (1999)
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BF128999 BF128999 1 GI:10968039 EST128990.1 GI:10968039
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CM2-ST0182-221099-023-f04
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                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (basel to 691)

NHH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapba-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CONA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
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96.8%; Pred. No. 5...
0; Mismatches
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db xref="taxon:9606"
<clone="IMAGE:4054205"</pre>
                                                                                                                                                                                                                                                                         High quality sequence stop: 682.
Location/Qualifiers
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Best Local Similarity 96.8
Matches 328; Conservative
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DEFINITION

AW406572

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/note="weetor: pT713-Pac, Site 1: Not1; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (L5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Benaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW404610 550 bp mRNA linear EST 16-FEB-2000 UI-HF-BL0-acc-a-06-0-UI INH MGC_37 Homo sapiens cDNA clone IMAGE:3058451 5', mRNA sequence.
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                               Euteleostomi;
                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Enc NI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
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                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleo
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Seg primer: M13 Forward.
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/cell_line="MGC85"
/lab_host="DH10B (LTI)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                         (bases 1 to 508)
                                                                                                                                                                                  Unpublished (1999)
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Matches 318; Conservative 0; Mismatches 21; Indels 0;
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                                                                                          Homo sapiens

Bukaryota, Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Lobases 1 to 550;

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MgC)

Contact: Robert Strausberg, Ph.D.

Eco RI site shown at the beginning of the sequence.

Contact: Robert Strausberg, M.B. Soares Lab

Eco RI site shown at the Beginning of the sequence.

CONA Library Preparation: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be distribution; MgC clone distribution information can be cond through the I.M.A.G.B. Consortium/Link at:

Seq primer: Mi3 Porward.

Location/Qualifiers

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Matches 318; Conservative 0; Mismatches 21; Indels 0; Gaps
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/lab host="Wetcor: pT713-Pac; Site 1: Not1; Site 2: Eco RI;
/note="Vector: pT713-Pac; Site 1: Not1; Site 2: Eco RI;
/note="Vector: pT713-Pac; Site 1: Not1; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 630)
                                                                                                                                                                                                                                                            Contract: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco II site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
Clone distribution: M.G. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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IMAGE:3060017 5', mRNA sequence.
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/db_xref="taxon:9606"
/clone="IMAGE:3060017"
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RESULT 12 BG426036

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BG426036 798 bp mRNA linear EST 14-MAR-2001
602492715F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4606658 5',
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1345 row: n column: 03
High quality sequence stop: 542.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:4606658"
/clone lib="NIH MGC 75"
/lab_host="DH10B_(TI phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Best Local Similarity 93.5%;
Matches 317; Conservative 0
                                                   mRNA sequence.
                                                                                                                                                                        Homo sapiens
                                                                                                                                              human.
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1L3-E70116-281000-308-H01 ET0116 Homo sapiens cDNA, mRNA sequence.
BF870122
BF870122.1 GI:12260252
BST.
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Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria,
Mammalia, Eutheria,
Masses 1 to 553)
Nagas Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Goldman, G.H., Carvalho, M.P., Mateukuma, A., Bordan, S., F.F.,
M.J., Soares, M. Galiveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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89.1%; Score 302.2; DB 12; Length 553;
Best Local Similarity 93.2%; Pred. No. 1.3e-81;
Matches 316; Conservative 0; Mismatches 23; Indels 0;
         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                        RESULT 14
BF870122/c
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                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db zerfe="Laxon:9606"
/clone="InAdE:4716948"
/clone_lib="NIH MGC 77"
/lab_lost="HIH10B (TI phage-resistant)"
/note="Organ: lung; Vector: pDNR-LnB (Clontech); Site 1:
Sfil (ggcgctcggcc); Site 2: Sfil (ggcattatggcc); 57 and
3/ adaptors were used in cloning as follows: 5/ adaptor
s-ATTCTAGAGGCCATATGGCC-3/ and 3/ adaptor sequence:
5/-ATTCTAGAGGCCACATGGCCCATG-dT(30)BN-3' (where B = A,
c, or G and N = A, C, C, G, or T). Average insert size 1:9
by PCR: This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
                                                                                                      **BGE59993
602590249F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4716948 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 149
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89.2%; Score 302.4; DB 12; Length 921;
Best Local Similarity 95.0%; Pred. No. 1.4e-81;
Matches 323; Conservative 0; Mismatches 16; Indels 1;
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181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGGGTCTGGGACAGATTTCACTCTCACC 240
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                                                                           371 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTATGGGACAGATTTCACTCTCACC 312
                                                                                                                                        ATCAGCAGCCTGCAGGCTGAAGATGTGGCCAGTTTATTACTGTCAGCAATATTATAGTACT 300
                                                                                                                                                                                                     311 ATCAGCAGCCTGCAGGCAGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATGCAACT 252
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           757 bp mRNA linear EST 21-MAR-602505173F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4618290 S'
BG484518
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                                                                                                                                                                                                                                                                      CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
                                                                                                                                                                                                                                                                                                               251 CCTCGGACGTTCGGCCAAGGGCCCAAGGTGGAAATCAAA 213
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206 TGGTACCAGCAGAAACCAGGACAGACTCCTAAACTGCTCATTTATTGGGCATCTACCCGG 265
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                                                                                                                                                                                                                                                                     326 ATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTCCT 385
                                                                                                                              266 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC
                                                                                            GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC
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DNA sequence of Hu Human Hum4L-CC49 V Sequence of pSC49F DNA sequence of pS

Plasmid pSC49FLAG Human Hum4 VL Clai Nucleotide sequenc

AAZ39432 ABQ56219

AAQ5673

10028 10028 10028 10028 10039

Plasmid pATDFLAG F Sequence of Hum4 V

AAQ45605 AAZ39436 AAZ23974

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Human ovarian anti Human cDNA clone H Sequence of Hum4VL Nucleotide sequenc Human monoclonal a

Sequence of plasmi Anti-TGF beta-1 sc Light chain DNA fr V-region of L-chai Human ovarian anti

AAA96146 AAX90025 AAQ56740 AAT60383 ABK24413 AAQ26047

AAA96134 AAA96150 AAA96158 AAA96138

AAA96140

AAQ45602

Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc Human HIV-1 monocl JP11.27855 Seq ID Sequence of the Hu Sequence of single Nucleotide sequenc Human SCFVI DNA.

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ALIGNMENTS

BP.

Noguchi H;

Nakatani T, Nomura N, Horigome K,

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Location/Qualifiers

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IgM antibody CEM 1

LNBOTDC vector #2
LNBOTDC vector #2

AAD28332

AAA96132

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Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region;
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87JP-0298513.
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26-NOV-1987;
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Listing first 45 summaries
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Noguchi H;

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New gene encoding for antibody to Pseudomonas aeruginosa exotoxin plus recombinant vectors and host cells, useful for treating infections.
                             Nomura N, Horigome K,
          (SUMO ) SUMITOMO CHEM IND KK.
                                                                                                              Disclosure; ; p; English.
                                                 WPI; 1988-156310/23
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                             New gene encoding for antibody to Pseudomonas aeruginosa exotoxin plus recombinant vectors and host cells, useful for treating infections.
                                                                                      Sequence encodes variable region of light chain of anti-exotoxin antibody. It encodes the same protein sequence as AAN80498 except that the signal sequence of AAN80498 contains an intron. See also AAN80495-N806496, AAN80498 and AAN80491-2.
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                                                                                                                                          Seguence 400 BP; 93 A; 109 C; 101 G; 97 T; 0 other;
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                                                                    Claim 5; page 27; 39pp; English.
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WPI; 1988-156310/23.
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Genomic DNA was isolated from the Epstein Barr virus-transformed human cell line FK001, fragmented and a gene library constructed. The library was screened with H or L chain probes and positive clones were identified including lambda gFK1. This clone contained an 11.58b insert encoding the V and C regions of Kappa chain. ECORI digested vector pSV2neo was end-filled and then blunt-end ligated to a Sall linker to form pSV2neoSall. This plasmid and pSV2neoGFK1 which was itself digested with Sall and ligated together to form pSV2neoGFK1 which was itself digested with Pvul. The plasmid was used to transform mouse myeloma cells which then expressed the antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGGACAGATTTCACTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                             New gene encoding for antibody to Pseudomonas aeruginosa exotoxin plus recombinant vectors and host cells, useful for treating infections.
                                                                                                                                                                                                                                                               Sequence encodes variable region of light chain of anti-exotoxin antibody. The signal sequence contains an intron which is spliced out prior to translation. See also AAN80495-N80496, AAN80499 and AAN80941-2.
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                           Query Match 96.2%; Score 326.2; DB 9; Length 619; Best Local Similarity 97.6%; Pred. No. 9.3e-95; Matches 331; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                          Sequence 619 BP; 177 A; 139 C; 134 G; 169 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccrccaacgrrccgccaagggaccaaggrgaaarcaaa 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccrcgracgricggccaaggaccaaggriggaarcaaa 618
                                                                                                                                                                  Nomura N, Horigome K, Noguchi H;
Location/Qualifiers
1..49
/*tag= a
269..279
560..268
/*tag= c
                                                                                                                                                                                                                                                Claim 5; page 26; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ33032 standard; cDNA; 342
                                                                                                                                                 (SUMO ) SUMITOMO CHEM IND KK
                                                                                                       87EP-0117760
                                                                                                                        86JP-0288340.87JP-0298513.
                                                                                                                                                                                   WPI; 1988-156310/23.
P-PSDB; AAP80894.
                                                                                                       01-DEC-1987;
                                                                                                                        03-DEC-1986;
26-NOV-1987;
                                                                                                                                                                  Nakatani T,
        sig_peptide
                           sig_peptide
                                                                                      08-JUN-1988
                                                                      EP270077-A
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ID AAQ3
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ATCAGCAGCCTGCAGCCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCCAACAATAAGAAATACTTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 IGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 dacarcergargaeceagrerecagaerecergeergrerereggegaggggegeeee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACATCCAGTTGACCCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A human MAb specifically binding to a surface antigen of cancer cell membrane comprises variable regions of the heavy and light chains having the amino acid sequences of AAR30143-44 respectively, encoded by DNA sequences AAQ38670 and AAQ33032 respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human monoclonal antibody specific for a cancer cell membrane surface antigen - prepd. from a hybridoma obtd. by cell fusion between human lymphocytes derived from cancer patients and mouse myeloma cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ë
                                                      Monoclonal antibody; hybridoma; PCR; variable region; constant region; heavy chain; light chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tagawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 342 BP; 88 A; 92 C; 87 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagaike K,
GAH variable region of light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 31 + 15; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hirakawa Y, Hosokawa S, Ito N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MITU ) MITSUBISHI KASEI CORP
                                                                                                                                                                                                                                                                                                                                                                                           91JP-0158859.
91JP-0158860.
91JP-0158861.
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                                                                                                                                                                                                                                                                                                                                     92EP-0110841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-001328/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR30144
                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-1991;
28-JUN-1991;
28-JUN-1991;
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AAQ71718
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240 240

(first entry)

06-MAY-1993

120 120 180 180

240 312

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121 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 180
                                                                                                            241 CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGATACTCCCCCCGACGTTC 300
                                                        181 CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCTG
                                                                                         CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCGAACGTTC
                             CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
                                                                                                                                                    GGCCAAGGGACCAAGGTGGAAATCAAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-066596/09.
P-PSDB; ABB07172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200185797-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rodriguez M,
                                                                                                                                                                                                                                                                                                                      13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2001.
                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                        ABA94219;
                                                                                         253
                                                                                                                                                    313
                             193
                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                            ABA94219
                                                                                                                 Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymphocytes were sepd. from regional lymph nodes of a patient who had undergone mastercomy for breast cancer. The Blymphocyte fraction was incubated for 20 hrs with Epstein-Barr virus, then cloned by limiting dilution and tested for immunoadherence. Clones producing antibodies reactive with the UCLA-SO-M12 melanoma cell line were recloned 7 times in serum-free medium contg. growth factors. The resulting L612 is a B-lymphoblascoid cell line transformed by the Epstein-Barr virus. It is deposited at the ATCC under CRL 10724. Humab L612 binds to renal cell carcinomas. The DNA sequence of the variable regions for both the light and heavy chains of the L612 antibody were determined by PCR and are given in AAQ71717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New transformed human B lymphoblastoid cell line - producing monoclonal antibody reactive with GM3 and GM4 ganglioside(s), for treating tumours, esp. melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery March
Best Local Similarity 98.5%; Pred. No. 1.5e-92;
Marches 322; Conservative 0; Mismarches 5; Indels C
                                          Monoclonal antibody L612 light chain variable region.
                                                                    Immunoglobulin, L612, light chain; variable region; monoclonal antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 360 BP; 88 A; 104 C; 85 G; 83 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 31-32; 39pp; English.
                                                                                                                                               Location/Qualifiers
1..360
/*tag= a
                                                                                                                                                                                                           /*tag= b
//label= CDR 1
154..174
/*tag= CDR 2
/label= CDR 2
271..297
                                                                                                                                                                                                                                                                                                      /*tag= d
/label= CDR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0026320.
                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US01469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                              58..108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-294324/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR61240.
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                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-1993;
                                                                                                                       Homo sapiens
                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1994,
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The invention provides a neuromodulatory agent (1) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in neurite outgrowth, regeneration, remyelination and neuroprotection in promoting callular proliferation of glial cells, and promoting Ca2+ signaling with oligodendrocytes. An humanised antibody to (1) can be selected from antibody sHIGM22 (LYM 22), ebyHigh MSI19D10, eby High CB2bG8, AKCR4, CB21E12, CB21E7 or NSI19ES. (1) is useful for stimulating remyelination of CNS axons, stimulating proliferation of glial cells in CNS axons, or treating demyelinating disease of CNS of such therapy. (1) is capable of binding to structures and cells within CNS axons or treating demyelinating disease of CNS of a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a cural disease of CNS (TMEV) (1) is also useful for an in vitro method of stimulating the proliferation of glial cells from mixed cell culture.
                                                                                                                                                                                                                                                           Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19B5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary; ds.
                                                                                                                                                                                                                     ebvHigM MSI19D10 light chain variable region nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel neuromodulatory agent (a human IgM monoclonal antibody) promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis
GGCCAAGGGACCAAGGTGGAAATCAAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MAYO-) MAYO FOUND MEDICAL EDUCATION RES
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..357
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miller DJ, Pease LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 43; Fig 20; 219pp; English.
                                                                                                          ABA94219 standard; DNA; 357 BP
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                                                                                                                                                                                     (first entry)
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132

9 72

61 TCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTACCTTGGTACCAGCAG 120 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 192

133

dd

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13 ACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 1 ACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGGAGGGCCACCATCAACTGCAAG 73 TCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTACCAGCAG

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2000-587534/55

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(I) is also useful for stimulating remyelination of CNS axons. The antibodies are useful for preventing infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition in a subject. Methods where (I) is administered to a patient are useful for treating multiple sclerosis, Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating disease, CNS diseases, and other conditions in the CNS
                                                                                                                                 The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                          ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT
                                                                                                                                                                                                                                                                                               1 GACATCCAGTTGACCCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                    GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                       ATCAACTGCAAGTCCAGAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAATCCGGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGATTTCACTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT
                                                                                                                             where nerves are damaged as by trauma. The present sequence represent
the ebvH1gM MSI19D10 light chain variable region nucleotide sequence
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; colon cancer; colon cancer antigen; diagnosis; detection; defactification; cytostatic; cardioactive; neuroprotective; vulner immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disoxder; immune system disorder; muscular disoxder; reproductive disoxder; qastrointestinal disoxder; reproductive disoxder; antihectious disease; cardiovascular disorder; se.
                                                                                                                                                                                                                     Query Match 93.9%; Score 318.2; DB 24; Length 357; Best Local Similarity 96.2%; Pred. No. 2.8e-92; Matches 326; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon cancer antigen nucleotide sequence SEQ ID NO:453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccrcrcacrrrcacccracaccaaacracaaa 339
                                                                                                                                                                                    Sequence 357 BP; 88 A; 101 C; 86 G; 82 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200055351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1999;
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AAC98443
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                                                                                                                                                                                                    human colon cancer antigens can have cytostatic, cardioactive, muscular, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnostics to the proteins are useful for the prevention, treatment and diagnostics of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, wounds, renal disorders, infectious disorders, and cardiovascular disorders. AAC98774 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                    Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer
                                                                                                                                                                      AAC97991 to AAC98763 encode the human colon cancer associated proteins
                                                                                                                                                                                            called human colon cancer antigens, given in AAB53234 to AAB54006. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 ATCAGCAGNCTGCAGGCTGAAGATGTGGCAGATTATTACTGTCAGCAATATTATACTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 463 BP; 106 A; 126 C; 113 G; 112 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cccrigaacerrcaeccacrigaaccaangragaarcana 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.0%; Score 315.2; DB 21; 95.3%; Pred. No. 2.8e-91; ive 0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA
                                                                                                                                 Claim 1; Page 935; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of seq Id No.
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nes 323; Conservative
                  P-PSDB; AAB53686
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                                                                                                                                                                                                                  The invention relates to producing gene libraries, comprising immunoglobulin light and heavy variable region. The method involves selecting light chain that binds with the heavy chain product to produce a functional conformation, producing a gene library comprising a collection of these light chain variable genes, and combining with gene library of heavy chain variable genes. The method is used for production of gene and antibody libraries.
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                                                                                                                                             Producing gene libraries and antibody libraries, involves selecting a
light chain that binds to a heavy chain product to produce a functional
formation, and producing a gene library of the light chain variable
                                                                                  Takahashi M;
                                                                                                                                                                                                                                                                                                                                                                    1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                      1 GACATCGTGATGACCCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single chain antibody; SCFV1; human subgroup 4 germline antibody; variable light; ss.
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of pATDFLAG encoding signal peptide, H4VL, linker and FLAG adapter.
                                                                                                                                                                                                                                                                                                                          Query March 92.9%; Score 315; DB 22; Length 360; Best Local Similarity 95.6%; Pred. No. 3e-91; Marches 324; Conservative 0; Mismatches 15; Indels 0
                                                                                 Shinohara M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccgracacriringeccagedeaccaaecreeacarcaaa 339
                                                                                                                                                                                                                                                                                                      Sequence 360 BP; 89 A; 100 C; 89 G; 82 T; 0 other;
                                                                                 Iba Y, Morino K,
                                                            (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
                                                                                                                                                                                                  Examples; p 147-148; 181pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ45606 standard; DNA; 1028 BP.
                    22-FEB-2001; 2001WO-JP01298
                                         2000JP-0050543
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                                                                                 Υ,
                                                                                Kurosawa Y, Akahori
Okuno Y, Shiraki K;
                                                                                                               WPI; 2001-565420/63.
P-PSDB; AAG65565.
                                         22-FEB-2000;
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30-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The plasmid pATGFLAG was generated from pSCFVUHH (see AAQ45605) to incorporate a flag-coating sequence 3' to any human VH gene to be expressed contiguously with Hum4 VL. The plasmid pATGFLAG, when digested with XhoI and Nhe I and purified becomes the human cH discovery plasmid contg. Hum4 VL in this SCFV format. pSC49FLAG contains murine antibody CC49VH inserted into sites of XhoI - hold purpose of pATDFLAG. It was evaluated for biological activity with the purpose of serving as a positive control for the FLAG assay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composite antibody binding to tumour associated TAG-72 antigen - includes light chain variable region from human subgroup 4 germline gene, useful, opt. as conjugate, for diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1028 BP; 289 A; 226 C; 244 G; 269 T; 0 other;
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                                                                 /note= "ENCODES SIGNAL, H4VL, LINKER see AAR38320 FT"
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                                                                                                                                              /*tag= c
/product= flag peptide
Location/Qualifiers
293..775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mezes PS, Richard RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                    (DOWC ) DOW CHEM AUSTRALIA LID
                                                                                                                                                                                                                                                                                                                                                                      91WO-AU00583.
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P-PSDB; AAR38320, AAR40753.
                                                                                                                       784..816
                                                *tag=
                                                                                                                                                                                                                                                                                                                      13-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                      13-DEC-1991;
                                                                                                                                                                                                                                                                        24-JUN-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson KS,
                                                                                                                                                                                                                     WO9312231-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY50693
                                                                                                                                                                                                                      09-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                              16-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                     19-APR-1990;
20-OCT-1992;
                                                                                                                                                                                                                                                                                                                                             US5976531-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson KS,
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                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                           599
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TAG-72; c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to producing humanized anti-tumor associated sialylated glycoprotein (TAG-72) antibodies (anti-TAG). The antibodies have binding specificity for the cancer antigen TAG-72. These antibodies have variable regions with VL segments derived from human subgroup IV germline gene and a VH segment (encoded by the VHalphaTAG germline gene) which is capapble of combining with the VL to form a threee dimensional structure having the ability to bind TAG-72. They can be used for the in vivo detection of carcinoma Tesons. They can also be used for the in vivo diagnostics. They can also be used for in vitro diagnostics. They can also be used for in vitro radionuclide, drug, biological response modifier, toxin or another antibody for the treatment of cancers. The humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                Production of humanized anti-TAG-72 antibodies, used for the detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                             Tumor associated sialylated glycoprotein; TAG-72; cancer antigen; carcinoma lesion; diagnostic; cancer; antibody; anti-mouse antibody hypersensitivity reaction; ss.
                                                                                                                      of Hum4 VL-UNIHOPE linker-FLAG peptide of pATDFLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1028 BP; 289 A; 227 C; 243 G; 269 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             in vivo imaging and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Fig 28A-C; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Mezes PS;
                                                ВР
                                               AAZ39437 standard; DNA; 1028
                                                                                                                                                                                                                                                                                            94US-0261354.
90US-0510697.
92US-0964536.
                                                                                                                                                                                                                                                                      95US-0487743
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Richard RA,
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-619651/53.
P-PSDB; AAY57184.
                                                                                                                                                                                                                                                                                                                                            (DOWC ) DOW CHEM CO.
                                                                                                                         DNA sequence
                                                                                                                                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                                                                                                                             16-JUN-1994;
                                                                                              29-FEB-2000
                                                                                                                                                                                                                    US5976845-A.
                                                                                                                                                                                                                                                                                                         19-APR-1990;
20-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                      Johnson KS,
                                                                                                                                                                                                                                             02-NOV-1999
                                                                                                                                                                                               Synthetic.
                                                                       AAZ39437;
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Matches
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300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; humanized; anti-tumor; sialylated glycoprotein antibody; cytostatic; cancer antigen; detection; carcinoma lesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel humanized anti-tumor associated stalylated glycoprotein antibodies (TAG-72) which have cytostatic activity. The antibodies have binding specificity for the cancer antigen TAG-72. They can be used for the in vivo detection of carcinoma lesions. They can also be used for in vitro diagnostics. They can also be modified with therapeutic agents e.g. a radiouclide, drug, biological response modifier, toxin or another antibody for the treatment of cancers. The humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACTAGGAATTTCACTCTCACC
                                                                                                                               241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanized anti-TAG-72 antibodies, used for the detection, in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                           CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
                                                                                                                                                                                                                                                               15;
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Pred. No. 9.7e-91;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; Figure 28A-C; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Richard RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pATDFLAG FLAG DNA adapter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 imaging and treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                             AAZ23975 standard; DNA; 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic; treatment; ss.
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Best Local Similarity 95.6
Matches 323; Conservative
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Gaps

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Indels

15;

418 120

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1 GACATCCAGTTGACCCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCCACC
                                Mismatches
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90US-0510697.
92US-0964536.
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson KS, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1994;
19-APR-1990;
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323;
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                                                                                    TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
             Plasmid pSCFV UHH expresses a biologically active, TAG-72 binding SCFV consisting of the Hum4 VL and CC49 VH. The expression plasmid utilises the beta-lactamase penP promoter, pectate lyase pelB signal sequence and the penP terminator region. Different Ig light chain variable regions can be inserted in the Ncol-HindIII sites, and different SCFV linkers can be inserted in the HindIII-XhoI sites and different Ig heavy chain variable regions can be inserted in the XhoI-Nhe I sites.
                                                                                                                                                                                                                                                                                             Single chain antibody; SCFV1; human subgroup 4 germline antibody; variable heavy; ss.
                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "ENCODES SIGNAL, H4VL, LINKER, CC49VH (SEE
AAR38319 FT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 314; DB 14; Length 1330;
Pred. No. 1.1e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composite antibody binding to tumour associated TAG-72 antigen - includes light chain variable region from human subgroup 4 germline gene, useful, opt. as conjugate, for diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1330 BP; 362 A; 300 C; 319 G; 349 T; 0 other;
                                                                                                                                                                                                                                                                      Sequence of Hum4 VL-CC49VH SCFV present in pSCFVUHH.
                                                                                                                                CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
                                                                                                                                                  Location/Qualifiers
293..1117
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                                                                                                                                                                                                                                                   (first entry)
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P-PSDB; AAR38319.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             Synthetic
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AAQ45605
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478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Production of humanized anti-TAG-72 antibodies, used for the detection, in vivo imaging and treatment of cancers
                                                                                                                                 539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTCACTCTACC
                                            599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAAGTTAT
181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGGGGGTCTGGGGACAGATTTCACTCTCACC
                                                                                                                                                                          241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor associated sialylated glycoprotein; TAG-72; cancer antigen; carcinoma lesion; diagnostic; cancer; antibody; SCFV; anti-mouse antibody hypersensitivity reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence of Hum4 VL-CC49VH SCFV present in pSCFVUIIII
                                                                                                                                                                                                                                         CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
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04-DEC-1993
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ID AAQ4
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                                                                                                                                                                                                                               GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                                                                                                                                     GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACC
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                                                                                                                                                                                             Gaps
diagnostics. They can also be modified with therapeutic agents e.g. radionucliae, drug, biological response modifier, toxin or another antibody for the treatment of cancers. The humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody hypersensitivity
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                                                                                                                                                     Length 1330;
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                                                                                                               Sequence 1330 BP; 362 A; 302 C; 317 G; 349 T; 0 other;
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                                                                                                                                                     Score 314; DB 20;
Pred. No. 1.1e-90;
                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                     Query Match
Best Local Similarity 95.6%;
Matches 323; Conservative
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92US-0964536
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Best Local Similarity
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This invention describes novel humanized anti-tumor associated sialylated glycoprotein antibodies (TAG-72) which have cytostatic activity. The antibodies have binding specificity for the cancer antigen TAG-72. They can be used for the in vivo detection of carcinoma leaions. They can also be used for in vitro diagnostics. They can also be modified with therapeutic agents e.g. a radionuclide, drug, biological response modifier, toxin or another antibody for the treatment of cancers. The humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                         Single chain antibody; SCFV1; human subgroup 4 germline antibody; variable heavy; ss.
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/note= "ENCODES SIGNAL,HV4L,LINKER,CC49VH,FLAG
- SEE AAR38321 FT"
                                                                                                                                                                                                                                                                                                                    Length 1330;
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                                                                                                                                                                                                                                                                 C; 317 G; 349 T; 0 other;
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                                                                                                                                                                                                                                                                                                               Score 314; DB 20;
Pred. No. 1.1e-90;
0; Mismatches 15;
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293..1147
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                                                                                                                                                                                                                                                                 Sequence 1330 BP; 362 A; 302
                                                                                                                                                                                                                                                                                                                    92.68;
                                                                                                                                                                                                                                                                                                                                          ilarity 95.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 323; Conserv
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The plasmid pATGFLAG was generated from pSCFVUHH (see AAQ45605) to incorporate a flag-coating sequence 3' to any human VH gene to be expressed contiguously with Hund VL. The plasmid pATGFLAG, when digested with XhoI and Nhe I and purified becomes the human chi discovery plasmid contg. Hund VL in this SCFV format. pSC49FLAG contains murine antibody CC49VH inserted into sites of XhoI - Apripase of pATPFLAG. It was evaluated for biological activity with the purpose of serving as a positive control for the FLAG assay
                                                                                                 New composite antibody binding to tumour associated TAG-72 antigen - includes light chain variable region from human subgroup 4 germline gene, useful, opt. as conjugate, for diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1359 BP; 374 A; 308 C; 325 G; 352 T; 0 other;
  Richard RA
                                                                                                                                                                                                      Example, Figure 30; 150pp; English
  Johnson KS, Mezes PS,
                                        WPI; 1993-214173/26.
N-PSDB; AAQ44607.
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GAATCCGGGGTCCCTGACCGATTCAGTGGCGGGGTCTGGGGACAGATTTCACTCTCACC 240 359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGCCCACC 418 61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120 419 ATCAACTGCAAGTCCAGGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180 GAATCCGGGGTCCCTGACCGATTCAGTGGCACGGGTCTGGGACAGATTTCACTCTCACC 598 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATTAT 658 ATCAGCAGCCTGCAGGCTGAAGATGTGGCCAGTTTATTACTGTCAGCAATATTATAGTACT 300 1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60 0; Gaps Ouery Match 92.6%; Score 314; DB 14; Length 1359; Best Local Similarity 95.6%; Pred. No. 1.1e-90; Matches 323; Conservative 0; Mismatches 15; Indels 0; CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338 121 599 181 539 241 301 g В q ð ò ò ò 임 ò a ò

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Search completed: July 18, 2003, 06:44:05 Job time : 88.8822 secs

13629, A 10845, A 13, Appl 57, Appli 7, Appli 5, Appli 5, Appli 21, Appl

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US-09-791-578-3 US-09-791-540-3

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Appl Appl

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US-09-187-693-28 US-09-828-708-112 US-09-604-287A-409 US-09-551-621-409 US-10-007-805-409 US-10-107-6622-409 US-10-107-662-409 US-10-121-464-5 US-10-121-464-1 US-10-121-464-1 US-10-121-464-1 US-10-121-464-1 US-10-121-464-1 US-10-121-464-1 US-10-121-464-1 US-10-136-846-10845 US-09-879-461-13 US-09-898-831-8 US-09-998-831-8 US-09-995-693-3 US-09-995-693-3 US-09-995-693-3 US-09-995-693-3 US-09-995-693-3 US-09-995-698-1 US-09-956-086-1

Sequence Sequence Sequence Sequence

Sequence 4 Sequence 4 Sequence 4

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Sequence 453, Application US/09925299;
Patent No. US20020055627A1;
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR RELING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556;
SOFTWARE: PATENTI Ver. 2.0
SEQ ID NO 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (453)
OTHER INFORMATION: n equals a,t,g, or
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LOCATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (393)
OTHER INFORMATION: n equals a,t,g, o)
NAME/KEY: misc feature
LOCATION: (404)
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NAME/KEY: misc feature
LOCATION: (453)
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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NAME/KEY: misc feature
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ORGANISM: Homo sapiens
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LOCATION: (435)
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Sequence 453, App
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8533.875 Million cell updates/sec
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                                                                                                                                                                                      1 gacatccagttgacccagtc......ggaccaaggtggaaatcaaa 339
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                                                                                                July 18, 2003, 06:19:39 ; Search time 81.9507 Seconds
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1: \cgn2_6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: \cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: \cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
4: \cgn2_6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
5: \cgn2_6/ptodata/1/pubpna/USO7 NEW PUB.seq:*
6: \cgn2_6/ptodata/1/pubpna/USO7 NEW PUB.seq:*
7: \cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
7: \cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
8: \cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
9: \cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
10: \cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
11: \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
12: \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
13: \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
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15: \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
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17: \cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
18: \cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19: \cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
11: \cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
12: \cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
13: \cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
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19: \cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
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            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-09-187-693-26
US-09-897-511A-34
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US-09-997-5128-1
US-09-274-163E-1
US-09-274-163E-1
US-09-274-163E-1
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US-09-187-693-24
US-09-187-693-24
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Maximum Match 100%
Listing first 45 summaries
                                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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APPLICANT: Young et al.
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APPLICANT: Young et al.
FILTIE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and All
FILE REPERENCE: POLO15P1
CURRENT APPLICATION NUMBER: US/09/799,514
CURRENT APPLICANTON NUMBER: PCT/US00/23662
PRIOR APPLICANTON NUMBER: PCT/US00-08-29
PRIOR APPLICANTON NUMBER: 06/152,248
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
SOFTWARE: PATENTION NOW: 19
SOFTWARE: PATENTION NOW: 20
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92.0%; Score 311.8; DB 10; Length
Best Local Similarity 95.0%; Pred. No. 5.9e-97;
Matches 322; Conservative 0; Mismatches 17; Indels
al Similarity 95.3%; Pred. No. 2.8e-98; 323; Conservative 0; Mismatches 16; Indels
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US-09-799-514-2
IS-09-990ence 2, Application US/09799514
; Patent No. US2002065220A1
; GENERAL INFORMATION:
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US-09-799-514-2
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Matches 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05883
FRIOR PILING DATE: 2000-03-08
FRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARR: Patentin Ver: 2.0
SEQ ID NO 453
LENGTH: 463
                                          Score 315.2; DB 10; Length
Pred. No. 2.8e-98;
0; Mismatches 16; Indels
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
LOCATION: (315)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (393)
OTHER INFORMATION: n equals a,t,g, or
LOCATION: (494)
OTHER INFORMATION: n equals a,t,g, or
LOCATION: (404)
OTHER INFORMATION: n equals a,t,g, or
LOCATION: (426)
LOCATION: (426)
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; Publication No. US20030040617A9
; GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (435)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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US-09-925-299-453
                                     Query Match
Best Local Similarity 95.3%;
Matches 323; Conservative
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US-09-925-299-453
  US-09-925-299-453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/09187693
Fatent No. US20020173629A1
GENERAL INFORMATION:
APPLICANT: Jakobovite, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Jaka Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
TITLE OF INVENTION: Growth Factor Receptor
FILE REFERENCE: Cell 4.20 CIP2.
CURRENT APPLICATION NUMBER: US/09/187,693
CURRENT FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1101440.8
US-10-158-646-58
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                                                                                                                        Sequence 58, Application US/10158646

Publication No. US20030073105A1

GENERAL IRFORMATION:
APPLICANT: Lasek, Amy K.W.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0030-1
CURRENT APPLICATION NUMBER: US/10/158,646

CURRENT APPLICATION NUMBER: 05/299

PRIOR FILING DATE: 2001-05-31

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PERL PROGRAM

SEQ ID NOS: 78

LENGTH: 788
                          370 CCGTACAGTTTTGGCCAGGGACCAAGCTGGAAATCAAA 408
301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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US-09-187-693-26
                                                                                                                    US-10-158-646-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                    89.4%; Score 303; DB 11;
95.4%; Pred. No. 4.4e-94;
tive 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INVOCATION:
GENERAL INVOCATION:
TITLE OF INVENTION: Expression Vectors
FILE REFERENCE: GALA-06415,
CURRENT APPLICATION NUMBER: US/09/897,006
CURRENT FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: 60/215,851
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 34
LENGTH: 9511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 GGCCAAGGGACCAAGGTGGAAATCAAA 339
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PRIOR APPLICATION NUMBER: 09/162,280
PRIOR FILING DATE: 1980-09-29
PRIOR PILING DATE: 1980-09-29
PRIOR PILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 34, Application US/09897006; Patent No. US20020106729A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(463)
CTHER INFORMATION: n = A,T,C or G
US-09-187-693-26
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.4
Matches 312; Conservative
                                                                                                                                                                                                            TYPE: DNA ORGANISM: human
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121 TGGTACCAGCAGAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCGGG 180
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86.8%; Score 294.4; DB 12; Length 305;
Best Local Similarity 98.0%; Pred. No. 3.4e-91;
Matches 298; Conservative 0; Mismatches 6; Indels 0;
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Fatent No. US2020137897A1
Fatent No. US2020137897A1
GENERAL INFORMATION:
FAPILICANT: STEVENS, Fred J.
APPLICANT: STEVENS, Fred J.
APPLICANT: RAFFEN, Mosematie
APPLICANT: RAFFEN, Mosematie
APPLICANT: RAFFEN, Mosematie
FILE REPRENCE: 051583/0224
CURRENT APPLICATION NUMBER: US/09/274,163E
FILE REPRENCE: 051583/0224
CURRENT APPLICATION NUMBER: US/09/274,163E
FRICR APPLICATION NUMBER: US/09/274,163E
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FRICR APPLICATION NUMBER: US/09/274,163E
FRICR APPLIC
                                                                                                                                               RESULT 8
US-09-995-529-5
Sequence 5, Application US/09995529
Sequence 5, Application No. US20030099655A1
Sequence 5, Application No. US20030099655A1
Sequence 5, Application No. US20030099655A1
Sequence 7, Application No. US2003009655A1
SEPLICANT: Huse, William D.
SAPPLICANT: Huse, William D.
SAPPLICANT: Huse, William D.
SELECONT: TANGE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUSE TO THOUS
                                               6000 GACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 6033
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; ORGANISM: Homo sapiens
US-09-995-529-5
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US-09-274-163E-1
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5703 CGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAA 5762
                                                                                                                                CCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCGGGGAATC 185
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| Sequence 34, Application US/09897511A
| Sequence 34, Application No. US20030092882A1
| Publication No. US20030092882A1
| GENERAL INFORMATION:
| APPLICANT: Breach! Robert
| APPLICANT: Breach! Robert
| APPLICANT: Breach! Robert
| APPLICANT: Block, Gregory
| TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
| TITLE OF INVENTION: WOMBER: US/09/897,511A
| CURRENT APPLICATION NUMBER: US/09/897,511A
| PRIOR PLING DATE: 2001-06.29
| PRIOR PLING DATE: 2001-06.29
| PRIOR FILING DATE: 2000-07-03
| SOFTWARE: PRECEDING DATE: 2001-06.29
| SOFTWARE: PARCHILING PARCHILING DATE: 2001-06.29
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          61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACTCTAAGAACTACTTAGCT 120
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patent No. US20020137897A1

GENERAL INFORMATION:

APPLICANT: WILKINS STEVENS, Priscilla

APPLICANT: WAFFEN, Rosemarie

APPLICANT: RAFFEN, Rosemarie

APPLICANT: SCHIFFER, Marianne

TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION

FILE REFERENCE: 051583/0224

CURRENT APPLICATION NUMBER: US/09/274,163E

CURRENT FILING DATE: 1999-03-22

PRIOR FILING DATE: 1999-01-17

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PARENTIN Version 3.1
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, OTHER INFORMATION:
US-09-274-163E-5
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Factor No. US20020137897A1
GENERAL INFORMATION:
APPLICANT: STEVENS, Fred J.
APPLICANT: WILKINS STEVENS, Priscilla
APPLICANT: RAFFEN Rosemarie
APPLICANT: RAFFEN Rosemarie
APPLICANT: RAFFEN Rosemarie
APPLICANT: RAFFEN ROSEMBRING
APPLICANT: RAFFEN ROSEMBRING
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APPLICANT: RAFFEN ROSEMBRING
APPLICANT: 1999-03-22
CURRENT APPLICATION NUMBER: US/09/274,163E
CURRENT FLING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: US 08/373,380
FRIOR PILING DATE: 1995-01-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 3
LENGTH: 343
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.larity 91.2%; Pred. No. 5.3e-90;
Conservative 0; Mismatches 30; Indels (
                                                                                                                                                           Score 292.6; DB 11; Legal No. 1.5e-90; Indels
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86.3%; Score 292.6; Sest Local Similarity 91.4%; Pred. No. 1.5e
Matches 310; Conservative 0; Mismatches
) ORGANISM: Escherichia coli
; FEATURE: NAME/KEY: CDS
; LOCATION: (1)..(342)
; OTHER INFORMATION:
US-09-274-163E-1
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LOCATION: (1)..(342)

OTHER INFORMATION:

US-09-274-163E-3
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Matches 309; Conserv
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US-09-274-163E-3
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87 TITATACAGCTCCAACAACAATACTTAACTTGGTACCAGCAGAAACCAGGACAGCC 146
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US-09-187-693-24

i Sequence 24, Application US/09187693

patent No. US20020173629A1

i GENERAL INFORMATION:

APPLICANT: Jakobovits, Aya

APPLICANT: Jakobovits, Aya

APPLICANT: Jakobovits, Aya

APPLICANT: Jia, Xiao-Chi

TILEO EN INVENTION: Human Monoclonal Antibodies to Epidermal

TILEO F. INVENTION: Human Monoclonal Antibodies to Epidermal

TILEO F. INVENTION: Human Monoclonal Antibodies to Epidermal

TILEO F. INVENTION: Human Monoclonal Antibodies to Epidermal

TILEO F. INVENTION: Human Monoclonal Antibodies to Epidermal

TILEO F. INVENTION: Human Monoclonal Antibodies to Epidermal

TILEO F. INVENTION: Human Monoclonal Antibodies to Epidermal

FILEO F. INVENTION: 1998-11-05

PRIOR APPLICATION NUMBER: US/09/187, 693

PRIOR APPLICATION NUMBER: 09/162, 280

PRIOR PILING DATE: 1998-09-29

PRIOR PILING DATE: 1998-09-29

PRIOR PILING DATE: 1999-09-26

NUMBER OF SEQ ID NOS: 75

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 456

TYPE: DAA
PRIOR APPLICATION NUMBER: 09/162,280
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 08/651,362
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 460
                                                                                                                                                                                        FEATURE:
NAMES/KEY: misc_feature
LOCATION: (1)...(460)
OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc_feature
LOCATION: (1) ... (456)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: human
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Best Local Similarity 92.4%; Pred. No. 1e-88;
Matches 314; Conservative 0; Mismatches 25; Indels 1; Gaps
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OTHER INFORMATION: Incyte ID No. US20030073105A1 1101440.15
FEATURE:
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Refer No. US20020173629A1

REFLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
FILE REFERENCE: Cell 4.20 CEP2
CURRENT APPLICANTON NUMBER: US/09/187,693

CURRENT FILING DATE: 1998-11-05
         RESULT 12

US-10-150-646-59

US-10-150-646-59

Sequence 59, Application US/10158646

Publication No. US20030073105A1

GERREAL INFORMATION:

APPLICANT: Lasek, Amy K.W.

APPLICANT: Sornasse, Thierry

TITLE REFERENCE: PA-0030-1 US

CURRENT APPLICATION NUMBER: US/10/158,646

PRIOR APPLICATION NUMBER: 002-05-29

PRIOR APPLICATION NUMBER: 6002-05-29

PRIOR APPLICATION NUMBER: 6002-05-29

PRIOR APPLICATION NUMBER: 6002-05-29

PRIOR APPLICATION NUMBER: 002-05-29

PRIOR APPLICATION NUMBER: 002-05-29

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PERL Program

SEQ ID NO 59

LENGTH: 1230
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7. LOCATION: 1143-1160
OTHER INFORMATION: a, t, c, g, or other
US-10-158-646-59
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US-09-187-693-22
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string OF INVENTION: Human Monoclonal Antibodies to Epidermal

string OF INVENTION: Human Monoclonal Antibodies to Epidermal

string Reference: Cell 4.20 CIP2

string APPLICATION NUMBER: US/09/187,693

current Priling DATE: 1998-09-29

serior APPLICATION NUMBER: 08/162,280

serior APPLICATION NUMBER: 08/162,280

serior APPLICATION NUMBER: 08/105,280

serior APPLICATION NUMBER: 08/1362

serior APPLICATION NUMBER: US/09/162,280

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                                                                             82.3%; Score 279; DB 11; Length 456; 93.2%; Pred. No. 8.3e-86; ive 0; Mismatches 21; Indels
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Best Local Similarity 92.6%; Pred. No. 6.6e-85;
Matches 289; Conservative 0; Mismatches 23; Indels
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; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
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                                                                         Query Match
Best Local Similarity 93.2
Matches 302; Conservative
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ORGANISM: human
US-09-187-693-24
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Db 121 CCTAAGCTGCTCATTTACTGGGCATCCGGGGATCCGGGGTCCTGACGGATTCAGT 207
Db 122 CCTAAGCTGTTTACTGGGCATCTGGGGATCCGGGGTCCTGTGACGTTCAGG 180
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Oy 268 GCAGTTTATTACTGTCAGCATATTATAGTACTCCTCGAAGGCTGAAGATGTG 240
Oy 268 GCAGTTTATTACTGTCACCATATTATAGTACTCCTCGAAGGCTCAAGGGACCAAG
Db 241 GCAGTTTACTTCTGTCACCAATATTATAGTACTCCTCGGACGTTCGGCCAAGGGACCAAG
Oy 328 GTGGAAATCAAA 339
Db 301 GTGGAAATCAAA 312
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RESULT 1
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(Ggn2_6/ptodata1/ina/PCTUS_COMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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20, Appl 20, Appl 20, Appl		50, Appl 50, Appl 50, Appl 5, Appli	103, App 3, Appli 1, Appli 31, Appl	35, Appl 7, Appli
Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence
US-08-470-110A-20 US-08:667-769A-20 US-08-940-371-20	US-08-63/-64/-20 PCT-US9S-17082A-20 US-08-467-420A-50 US-08-470-110A-50 US-08-667-769A-50	US-08-940-371-50 US-08-637-647-50 PCT-US95-17082A-50 US-09-301-593-5	US-09-301-593-103 PCT-US93-08435-3 US-09-301-593-1 US-09-301-593-31	US-09-301-593-35 US-08-724-752-7
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ALIGNMENTS

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USE-OBE-160-125

Sequence 4. Application US/08360125

Patent No. 5767246

GENERAL INFORMATION

APPLICANT: Saiko HOSOKAWA

APPLICANT: Tobhiaki TAGAWA

APPLICANT: Wo. 5767246

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APPLICANT: Wo. 5767246

APPLICANTON: Working Tobhiaki TAGAWA

APPLICANTON WHORES:

COUNTRY: Washington

STATE: D.C.

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APPLICANT: Nearuhis of 1992
TITLE OF INVENTION: Gell Membrane
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FRAGENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
HAPLOTYPE:
TISSUE TYPE:
TISSUE TYPE:
CELL TYPE:
ANDIA SOURCE:
ORGANISM:
CELL INE:
ORGANISM:
CLONE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
CHROMOSOME/SEGMENT:
MAP POSITION:
WAP POSITION:
UNTES:
FEATURE:
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IDENTIFICATION METHOD:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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HYPOTHETICAL:
ANTI-SENEE;
ANTI-SENEE;
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL TYPE:
CELL TYPE: antibody GAH
CELL TYPE: antibody GAH
CELL TYPE: AND ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CIONE:
POSTITION IN GENOME:
CHROMOSOME/GEGMENT:
MAP POSTITION:
WAP POSTITION:
UNITS:
IDENTIFICATION METHOD:
OTHER INPORMATION:
PUBLICATION:
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS:
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-4
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US-08-450-578-4
; Sequence 4 Application US/08450578
; Patent No. 5837845
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Patent No. 5990297

GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack, L.L.P.
                                                                                                                                                                                                                                                                                                         1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
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IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/360,125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
                          GACATCCAGTTGACCCAGTCTC
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TELECOMMUNICATION INFORMATION
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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APPLICANT: HOSORAWA, Toshiaki
APPLICANT: HRAGAWA, Toshiaki
APPLICANT: HRAGAWA, Yoko
APPLICANT: HRAGAWA, Yoko
APPLICANT: ITO, No. 59902871hiko
APPLICANT: ITO, No. 59902871hiko
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT FILING DATE: 1998-02-02
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                       1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCCGAGAGGGCCACC
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US-09-017-628-4
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96.8%; Pred. No. 2.9e-97;
live 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                     Score 321.4; DB 2;
Pred. No. 2.9e-97;
                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                   DOCUMENT NUMBER:
FILING DATE:
RELEATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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Patent No. 5990287
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     94.8%;
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Best Local Similarity 96.8
Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                               Conservative
PUBLICATION INFORMATION AUTHORS:
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Best Local Similarity
Matches 328; Conserv
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ORGANISM: Unknown
                                              TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-017-628-4
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                                                                                  VOLUME:
ISSUE:
PAGES:
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: Hybridoma producing human
CELL TYPE: Antibody GAH
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PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-4
NAME: Warren M. Cheek, Jr.
REGISTRATION UNDHBER: 33,367
REFERENCE/DOCKET UNDHBER: TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPAX:
INFORMATION: 4:
SEQUENCE CHARACTERISTICS: LENGTH: 342 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
PRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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APPLICANT: Saiko HOSCKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: No. 6436434ihiko ITO
APPLICANT: No. 6436434ihiko ITO
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APPLICANT: No. 6436434ihiko ITO
APPLICANT: No. 6436434ihiko ITO
APPLICANT: No. 64364363
ADDRESSE: Wenderoth Lind & Ponack
STATE: D.C.
COUNTRY: U.S.A.
STATE: D.C.
COUNTRY: U.S.A.
COMPUTER: BADABLE FORM:
MEDJUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATION TO BATE: No. 530
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 03360
FILING DATE: December 20, 1994
PRIOR APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
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APPLICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGGGGTCTGGGACAGATTTCACTCTCACC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGCCACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
                                                                                                                                                                                                                                                                                                             Query Match 94.8%; Score 321.4; DB 2; Length 342; Best Local Similarity 96.8%; Pred. No. 2.9e-97; Matches 328; Conservative 0; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
         TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-450-363-4; Sequence 4, Application US/08450363; Patent No. 6436434
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US-09-014-880-4
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LOCATION: 154..174
OTHER INFORMATION:
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Best Local Simil
Matches 323; (
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241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
                                                               241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "HuMab L612 Light Chain Variable Region"
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Irie, Reiko F
TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
TITLE OF INVENTION: SCRETING ANTI-GANGLIOSIDE ANTIBODY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poms, Smith, Lande & Rose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Epstein Barr Virus transformed B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function= "Immunoglobulin light
                                                                                                                                                301 ccgregacerregeccaaegaccaaegregaarcaaa 339
                                                                                                        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function= "Complementary
determining region 1 (CDR1)"
                                                                                                                                                                                                                                                                                                                                                                                                                  E: Poms, Smith, Lande & Rose
2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNER: COURT PARK East, Suite CITY: Los Angeles STREET: California COUNTRY: United States of America ZIP: 90067

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Floppy disk COMPUTER: Floppy disk COMPUTER: Floppy disk COMPUTER: PROGREET: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/026,320A FILING DATE: 26-FEB-1993

CLASSIFICATION DATA: APPLICATION NUMBER: US 07/609803

FILING DATE: OS-NOV-1990

ATTORNEY/AGRAT INFORMATION: NAME: Oldenkamp, David J
                                                                                                                                                                                                                             US-08-026-320A-3
; Sequence 3, Application US/08026320A
; Patent No. 5419904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 360 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3107885046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 58..108
OTHER INFORMATION: /funct
OTHER INFORMATION: detert
FEATURE: MAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Epst
INDIVIDUAL ISOLATE: cell
CELL TYPE: B-cell
CELL LINE: L612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1.360
OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY:
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121 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGGTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTACCAGCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCGGGAATCCGGGGTC 192
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APPLICANT: Richard, Ruth A.
APPLICANT: Richard, Suth A.
APPLICANT: Richard, Joseph A.
APPLICANT: Kaffolter, Joseph A.
APPLICANT: Kaffolter, Joseph A.
APPLICANT: Kaffolter, Joseph A.
APPLICANT: Kaffolter, Joseph A.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
LENGTH: 1330
                                                                                                                                                                                                                                                                                                                                                                                                                 13 ACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG
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                                                                                                                                                                                                                                                                               Query Match 94.1%; Score 319; DB 1; Length 360; Best Local Similarity 98.5%; Pred. No. 1.9e-96; Matches 322; Conservative 0; Mismatches 5; Indels
/function= "Complementary
determining region 2 (CDR2)"
                                                                                                                                                        /function= "Complementary
determining region 3 (CDR3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 314; DB 3;
Pred. No. 1.6e-94;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 GGCCAAGGGACCAAGGTGGAAATCAAA 339
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NAME/KEX: HUMAVL-VH SCFV from pSCFV UHH

" LOCATION: 1..1330
US-08-463-903-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-463-903-5; Sequence 5, Application US/08463903; Patent No. 6071515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.6%;
ilarity 95.6%;
Conservative
                                                        FEATURE:

NAME/KEY: misc_feature

COCATION: 271..297

OTHER INFORMATION: /funct

COTHER INFORMATION: detern

US-08-026-320A-3
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US-08-463-903-19

US-08-463-903-19

Sequence 19, Application US/08463903

Patent No. 6071515

GENERAL INFORMATION:

APPLICANT: Meses, Peter S.

APPLICANT: Richard, Ruth A.

APPLICANT: Richard, Ruth A.

APPLICANT: Richard, Ruth A.

APPLICANT: Affolicer, Joseph A.

APPLICANT: Affolicer, Joseph A.

TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides

FILE REFERENCE: 40224A US

CURRENT FILING DATE: 1995-6-6-05

CURRENT FILING DATE: 1995-6-05

EARLIER FILING DATE: 1992-08-21

NUMBER OF SEO ID NOS: 102

SOFTWARE MS-WOR' FOR Windows, Ver. 7.0

LENGTH: 1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/07935695
Sequence 19, Application US/07935695
Sequence 19, Application US/07935695
Sequence 19, Application
APPLICANT: Mcass, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Affolier, Joseph A.
APPLICANT: Mcitte, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 402244 US
CURRENT FILING DATE: 1992-08-13
PRIOR APPLICATION NUMBER: US 08/463,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGGGGTCTGGGACAGATTTCACTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTCTGGGCGAGAGGCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA-
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pATDFLAG
LOCATION: 1..1027
US-08-463-903-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 1027;
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659 CCTCTCACTTTCGGCGGAGGACCAAGGTGGTGGTCAA 696
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US-07-935-695-19
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## Sequence 5, Application US/07935695

## Sequence 5, Application US/07935695

## Sequence 5, Application US/07935695

## Sequence 6, Application US/07935695

## SPECIAL INFORMATION:

## APPLICANT: Affholter, Joseph A.

## APPLICANT: Affholter, Joseph A.

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## APPLICANT: Affholt
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NAME/KEY: Hum4VL-VH scFv from pSCFV UHH
COCATION: 1...1330
SCHER INFORMATION: :
US-07-935-695-5
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ORGANISM: Artificial Sequence
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Query Match
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Fatent No. 6071515
Fatent No. 6071515
GENERAL INFORMATION:
APPLICANT: Mczes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Richard, Ruth A.
APPLICANT: Richolter, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REPERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT PILING DATE: 1995-06-05
BARLIER APPLICATION NUMBER: US 07/935,695
FARLIER PILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE MS-Word for Windows, Ver. 7.0
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PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 102
SOFTWARE: NS-Word for Windows, Ver. 7.0
SEQ ID NO 19
LENGTH: 1027
TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
NAME: WINHOPE linker-FLAG peptide construct in patDFLAG
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                                                                                                                                                                                                      Length 1027;
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Pred. No. 6.2e-93;
0; Mismatches 18;
                                                                                                                                                                                                      92.2%; Score 312.4; DB 4
95.3%; Pred. No. 4.7e-94;
live 0; Mismatches 16
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Best Local Similarity 94.7%;
Matches 320; Conservative
                                                                                                                                                                                                  92.27
Best Local Similarity 95.37
Matches 322, Conservative
                                                                                                                                                        , OTHER INFORMATION: :
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LENGTH: 1361
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US-08-463-903-21
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WS-07-935-695-21

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Sequence 21, Application US/07935695

Patent No. 632507

GENERAL INFORMATION:

APPLICANT: Mazes, Peter S.

APPLICANT: Richard, Ruth A.

APPLICANT: Richard, Ruth A.

APPLICANT: Richard, Ruth A.

APPLICANT: Affolice, Nicolas J.

TILE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides

FILE REFERENCE: 40224A US

CURRENT PILING DATE: 1992-08-21

PRIOR APPLICATION NUMBER: US/07/935,695

CURRENT FILING DATE: 1995-06-05

NUMBER OF SEQ ID NOS: 102

SOFTWARE: MS-Word for Windows, Ver. 7.0

SEQ ID NO 21

SEQ ID NO 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCTCACTTTCGGCGGAGGACCAAGGTGGTGGTCAA 696
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Pred. No. 6.2e-93;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.2%;
ilarity 94.7%;
Conservative
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OTHER INFORMATION: :
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Gaps

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967 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 1026
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APPLICANT: Richard, Ruth A.
APPLICANT: Afchard, Ruth A.
APPLICANT: Afchard, Ruth A.
APPLICANT: Afchier, Joseph A.
APPLICANT: Afchier, Nicolas J.
TILE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT APPLICATION NUMBER: US 07/935,695
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
WUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            847 IGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT
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0
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.0%; Score 308.6; DB 4; Length 1088; Best Local Similarity 94.4%; Pred. No. 8.9e-93; Matches 320; Conservative 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 836;
                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001
US-07-935-695-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 1.6e-90;
0; Mismatches 19;
CURRENT APPLICATION NUMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 3
LEMOTH: 1088
TYPE: DNA
ORGANISM: HOMO Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08463903
Patent No. 6071515
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 94.3%;
Matches 313; Conservative
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NAME/KEY: SCFV1 from pCGS515;
LOCATION: 1..836
US-08-463-903-1
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US-08-463-903-1
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   599 ATCAGCAGCCTGCAGGCTGAAGATGCGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658
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APPLICANT: Richard, Ruth A.
APPLICANT: Richard, Ruth A.
APPLICANT: Afforbler, Joseph A.
APPLICANT: Kotite, Mcoolss J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                        of Single Chain Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  847 IGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG
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NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001
1. LOCATION: 1..1088
19.08-463-903-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
91.0%; Score 308.6; DB 3; Length
Best Local Similarity 94.4%; Pred: No. 8:9e-93; Matches 320; Conservative 0; Mismatches 19; Indels
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                                                   301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
                                                                                                      659 cererederriegecegaegaeceaaggregareaa 696
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APPLICANT: Macses, Ruth A.
APPLICANT: Richard, Ruth A.
APPLICANT: Affholter, Joseph A.
APPLICANT: Kotite, Nicolas J.
ITLE OF INVENTION: Dimer and Multimer Forms of FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/08/463,903
CURRENT APPLICATION NUMBER: US/08/463,903
EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER APPLICATION NUMBER: US 07/935,695
SERLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-WORD for Windows, Ver. 7.0
SEQ ID NO 3
                                                                                                                                                                                                                                    Sequence 3, Application US/08463903
Patent No. 6071515
GENERAL INFORMATION:
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US-07-935-695-3
; Sequence 3, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1088
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US-08-463-903-3
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qq	77 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTTTTTTTT
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QQ	137 ATCAACTGCAAGTGCAAGGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 196
ò	121 TGGTACCAGCAGAAACCAGGACGAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
qa	197 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCGG 256
δλ	181 GAATCCGGGGTCCCTGACCGATTCAGTGGCGGGTCTGGGACAGATTTCACTCTCACC 240
qq	257 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC 316
ò	241 ATCAGCAGCTGCAGGCTGAAGATGTGGCAGTTTATTACTGCAGCAATATTATAGTACT 300
qa	317 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 376
ò	301 CCTCGAACGTTCGGCCAAGGGGGGGGGG332
qα	377 CCTCTCACTTTCGGCGGAGGGACCAGGTGAA 408
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Search completed: July 18, 2003, 19:59:07 Job time: 18:9759 secs

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July 18, 2003, 04:46:48; Search time 1030.02 Seconds (without alignments) 10397.705 Million cell updates/sec
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1 aggtgcagctggtgcagtct......ccctgctcatcgtctcctca 368
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1 7	2.662		369		HIMI GMR FK	I.19288 Homo sapien
13	297.4		429	n 01	HSZ80853	
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21	296.8		369	N	AF527046	046 Synth
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24	296.4		510	י ס	HS203E6	H.sapien
25	296.4		510	6	HS203E7	H. sapiens
26	296.4		510	σ	HS203E9	H.sapiens
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4.5	σ	79.1	н	σ	HSU84163	U84163 Homo sapien

ALIGNMENTS

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IgG CLL suggest selection for distinct surface membrane Ig
teceptors
Lumphlished (2 (bases 1 to 370)

RS Chioraczi, N.
Direct Submission

AL Submitted (02-SEP-1997) Medicine, North Shore University Hospital,
350 Community Dive, Manhasset, NY 11030, USA
Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Gualifiers

Location
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428 bp mRNA linear PRI 08-MAY-2001
Homo sapiens clone 2lu-19 immunoglobulin heavy chain variable
region (IGH) mRNA, partial cds.
AF062105
AF062105.1 GI:3170672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Homo sapiens

Bukaryotains

Bukaryotai, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,

Mammalia; Buthoria; Primates; Catarrhini; Hominidae; Homo.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.7%; Score 315.2; DB 9; Length 370; Best Local Similarity 91.0%; Pred. No. 1.4e-85; Matches 335; Conservative 0; Mismatches 33; Indels 0.
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362 TCTCCTCA 369
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Homo sapiens ID:CLL008 IgM heavy chain variable region mRNA,
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Homo sapiens
Homo sapiens
Fukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1] (bases I to 370)
Chiorazzi,N.
Differences in Ig variable region gene use and mutation in IgM vs
       Manheimer-Lory, A., Katz, J.B., Pillinger, M., Ghossein, C., Smith, A. and Diamond, B.
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100.0%; Score 368; DB 9; Length 368;
Best Local Similarity 100.0%; Pred. No. 8.9e-102;
Matches 368; Conservative 0; Mismatches 0; Indels
                                                               Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype J Exp. Med. 174 (6), 1639-1652 (1991) 92.078875 1660528
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                                                                                                                                                                                                                  1 (bases 1 to 525)

Kipps, T.J. and Duffy, S.F.
Relationship of the CD5 B cell to human tonsillar lymphocytes that express autoantibody-associated cross-reactive idiotypes
J. Clin. Invest. 87 (6), 2087-2096 (1991)
91250563
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                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L22, subgroup VH-I.
                                                                       V-region; immunoglobulin heavy chain subgroup VH-I; rearranged Homo sapiens tonsil DNA.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="14q22.33"
/cell_type="B lymphocytes"
/tissue_type="tonsil"
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/note="G00-118-731"
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/note="G00-118-731"
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/product="immunoglobulin heavy chain variable region"
/protein_id="AAC18141.1"
/db_xrein_id=1170673"
/translation="MDWTWRFIFTVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTFSSYAISWVRQAPQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMEL
SSLRSEDTAVYYCARDRVSGGSGYNWFDPGAREPWSPSPQG"
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9027689
2 (bases 1 to 428)
2 (bases 1 to 428)
Nang,X. and Stollar,B.D.
Direct Submission Partment, Tufts University
Submitted (22-APR-1998) Biochemistry Department, Tufts University
School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
Location/Qualifiers
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  Immunoglobulin VH gene expression in human aging Clin. Immunol. 93 (2), 132-142 (1999) 99459182
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Pred. No. 2.3e-84;
0; Mismatches 28
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/db_xref="taxon:9606"
/chromcosome="14"
/map="1432.33"
/clone="21u-19"
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ilarity 92.1%;
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/gene="IGH"
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Matches 339; Conserv
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Homo sapiens isolate HOW IgM heavy chain VH1 region precursor (VH1-69) gene, partial cds.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Cararthini; Hominidae; Homo.
I (bases 1 to 512)
Johnson, T.A., Rassenti, L.Z. and Kipps, T.J.
Ig Will genes expressed in B cell chronic lymphocytic leukemia exhibit distinctive molecular features
J. Immunol. 158 (1), 235-246 (1997)
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Johnson, T.A.
Direct Submission
Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, 3011a, CA 92093, USA
Jolla, CA 92093, 105A
1. 512
                                                                  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
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/note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
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CDN31B8).
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                          747233.1 GI:1197314

Homenroglobulin; immunoglobulin heavy chain; variable region.

Home sapiens

Buhen sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarthini; Hominidae; Homo.

1 (bases I to 113)

Demaison, C., David, D.; Letourneur, F., Zouali, M., Saragosti, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
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/db_xxef="kexon:906"
/clone="CDNJ1BB"
/call type="B-lymphocyte"
/tissue_type="peripheral blood lymphocyte"
/dev_stage="adult"
1.55
1.57
58. .456
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Pred. No. 3.9e-83;
0; Mismatches 38; Indels
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/product="immunoglobulin variable region"
111 c 142 g 84 t
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515 CCGTCTCCTCA 525
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/codon_start=1
/product="IgM heavy chain VH1 region precursor"
/protein_id="ABC51707.1"
/db_xref="GI:2344954"
/translation="MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1521 bp DNA linear PRI 27-AUG-1997
Homo sapiens isolate LID IgM heavy chain VH1 region precursor
TH84100
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1 (bases 1 to 521)
1 (bases 1 to 521)
1 (bases 1 to 521)
1 (but genes expressed in B cell chronic lymphocytic leukemia exhibit distinctive molecular features
J. Imminol. 158 (1), 235-246 (1997)
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Johnson, T.A.
Direct Subsassion
Submitted (088-JAM-1997) Medicine, UCSD, 9500 Gilman Drive, 0663,
Jolla, CA 92093, USA
                                                                                   145 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
                                                                                                                                                                                                              ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG
                                                 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
           Gaps
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/db_xref="taxon:9606"
/map="14932"
/note="CLL: chronic lymphocytic leukemia"
             Indels
           38;
           Mismatches
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/gene="VH1-69"
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             Conservative
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B (1) (Bases 1 to 515)

B Bahler, D.W., Miklos, J.A. and Swerdlow, S.H.
Ongoing Ig Gene Hypermutation by Salivary Gland Mucosa-Associated Lymphold Tissue-Type Lymphomas

Lymphold Tissue-Type Lymphomas

E (1997) In press

E (1997) In press

B Bahler, D.W., Miklos, J.A. and Swerdlow, S.H.

S Bahler, D.W., Miklos, J.A. and Swerdlow, S.H.

Direct Submission

L Submitted (26-NOV-1996) Pathology, Montefiore University Hospital, 200 Lothrop Street, Pittsburgh, PA 15213-2582, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSU79581 515 bp DNA linear PRI 01-FEB-1997
Human clone OR immunoglobulin heavy chain gene, partial cds.
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GGTFSTYAISWVRQAPGQGLEWMGGIIPIFGTANHAQKFQGRVTITADESTSTAYMEL
SSLRSEDTAVYYCAREGYDSSGSPKPFDYWGQGTLVTVSSG"
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                                                                                     AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
                                                                                                                                                                      CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG
                                                                                                                                                                                                                                                                                 CACAGAAGTICCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGGCACAGCCTACA
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protein id="AAB41736.1"
db_xref="G1:1813666"
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Pred. No. 3.9e-83;
                            38;
         89.7%; Pred. No. 3.9e-83;
:ive 0; Mismatches 38
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db_xref="taxon:9606"
chromosome="14"
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89.7%;
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       al Similarity 89.7
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TCTCCTCA 512
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/partial
/gene="Id@"
/codon start=1
/product="Ig heavy chain"
/product="Ig heavy chain"
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GGTFSSYAISWTRQAPGGGLEWMGGIIPIEGTANYAQKFOGRVTITADESTSTAYMEL
SSLRSEDTAVYYCARGGMGYCSGGSCYWFDPWGQGTLVTVSS"
join(11. .56,143. .153)
/note="G00-118-731"
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Catarrhini, Hominidae, Homo.
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83.0%; Score 305.6; DB 9;
Best Local Similarity 90.6%; Pred. No. 1.2e-82;
Matches 339; Conservative 0; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="IGH@"
/note="G000-118-731"
143. :528
/gene="IGH@"
/product="Ig heavy chain"
/note="G00-118-731"
a 131 c 170 g 119 t
                                                                                                                                                                                                                                                                                                                                                   <11. .56
/gene="IGH@"
/product="Ig heavy chain"
/note="G00-118-731"</pre>
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 387)
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GGTFSSYAISWVRQAPGGGLEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAYMEL
SARREBETAYYYYCASNEVTIFGVVIKTNWFDFWGQGTLVTVSS"
join(1. .46,133 .143)
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Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L42,
M65104
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M65104.1 GI:185344
Wregion; immunoglobulin heavy chain subgroup VH-I; rearranged DNA. Homo sapiens tonsil DNA.
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (Basas I to 528)
Kripps T.J. and Duffy.S.F.
Relationship of the CD5 B cell to human tonsillar lymphocytes that express autoantibody-associated cross-reactive idiotypes
J1250563
Clin. Invest. 87 (6), 2087-2096 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         204
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                                                                                                                                                                                                                                                                                               Length 521;
                                                                                                                                                                                                                                                                                               Query Match 83.1%; Score 305.8; DB 9; Length Best Local Similarity 90.5%; Pred. No. 1.1e-82; Matches 31; Conservative 0; Mismatches 27; Indels
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1. .528
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/tissue_type="tonsil"
11. .528
/gene="IGH@"
join(11. .56,143. .528)
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/translation="MDWTWRFLFVVAAATDVQSQVQLVQSGAEVKKPGSSVKVSCKAS
GGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMEL
SSLRSEDTAVYYCASCGSGSYWPLCNWFDFWGQGTLVTVSS"
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                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 515).

19 WH genes expressed in B cell chronic lymphocytic leukemia exhibit distinctive molecular features J. Immunol. 158 (1), 235-246 (1997)
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                                                                                                                                                                                                                                                                                             Johnson, T.A.
Direct Submission
Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663,
Jolla, CA 92093, USA
Location/Qualifiers
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/note="FW1/CDR1/FW2/CDR2/FW4"
130 c 163 g 117 t
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/isolate="patient LAN"
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/gene="VH1-69"
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/gene="VH1-69"
144. .515
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:9606"
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     (VH1-69) gene, partial cds.
U84178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .515
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                                          U84178.1 GI:2344949
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LEWMGGIIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARQADC
SGGSCYDIFPNWFDPWGQGTLVTVSSG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGACAAGCCG 301
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product="launoglobulin heavy chain variable region"
protein id="AAC18225.1"
/db_xref="GI:3170841"
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Homo sapiens isolate LAN IgM heavy chain VH1 region precursor
                                                                                                                                                       Department, Tufts Ur
., Boston, MA 02111,
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Whang, X. and Stollar, B.D. Immunoglobulin VH gene expression in human aging Clin. Immunol. 93 (2), 132-142 (1999)
                                                                                                                                                                                                                                                                                                                      cell_type="peripheral B lymphocyte"
tissue_type="blood"
note="from elderly repertoire 48u"
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Wang, X. and Stollar, B.D.
Submission
Submitted (22-APR-1998) Biochemistry Del
School of Medicine, 136 Harrison Ave.,
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89.8%;
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/gene="IGH"
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TGLNWFDFWGGGTLLVTSS"
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Human immunoglobulin heavy chain variable region (clone Tmu60)
mRNA, partial cds.
U00583
U00583.1 GI:392755
                                                                                                                                                                                                     297
                                                                                     181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCTACA 240
                                                                                                                                             241
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 363)

Huang, C. and Srollar, B.D.

Am ajority of 1g H chain cDNA of normal human adult blood

lymphocytes resembles cDNA for fetal Ig and natural autoantibodies
CTGGACAAGGGCTTGAGTGGATGGGAAGGATCCTTCCTTGGTATAGCAAACTACG 181
                                                                                                                                                                                                                                  242 TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGATGCCATA 301
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                                                                                                                      182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
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Stollar, B.D.
Direct Submission
Submitted (10-A0G-1993) Stollar B.D., Tufts University,
Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 363;
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/tissue_type="peripheral blood"
/clone_lib="Tmu"
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human.
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AB067158 I GI:21670372
298 CCGATTATGTTTTGGGGGAGCGACTAGTTCGACCCCTGGGGCCAGGAAACCTGCTCA 357
445 CGGGGAGTTATTGGCGTTTGTGCATTTTGTGACCCTGGGGGCAAGGAAACCCTGGTGA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.

Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:ya0037h.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Immunology; Kutsukake-cho, Toyoake, Aichi 470-1192, Japan (Email:kurosawa@tujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 372;
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Pred. No. 7.5e-82;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="AlmS4"
/note="mixture of tissues:tonsils,
peripheral blood and bone marrow"
1. 372
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/db_xref="taxon:9606"
/clone="ya0037h"
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89 c 115 g
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Best Local Similarity 91.0%;
Matches 334; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
2 (bases 1 to 372)
                                                                                                                                             505 CCGTCTCCTCA 515
                                                                                                               358 TCGTCTCCTCA 368
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AB067158
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518 bp DNA linear PRI 27-AUG-1997
Homo sapiens isolate CRA 1gM heavy chain VH1 region precursor
(VH1-69) gene, partial cds.
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1 (bases I to 518)
Johnson, T.A., Rassenti, L.Z. and Ripps, T.J.
IG VH1 genes expressed in B cell chronic lymphocytic leukemia exhibit distinctive molecular features
J. Immunol. 158 (1), 235-246 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 518)
Johnson, T.A.
Johnson, T.A.
Submitted (Une-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, Jolla, CA 92093, USA
                                                                                                                                                                                                                                                                                                    385 IGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445 GTAGTGGTGGTAGTTGTTTTGGGGCTGGTTCGACCCCTGGGGGCCAGGGAACCCCTGG
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                                                                                                                                                                                                                                                                                                                                                                         145 AGGTGCAGCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
                                                                                                     ;
                                                                     518;
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/note="CLL: chronic lymphocytic leukemia"
                                                                     Length
                                                                                                     Indels
                                                                                                                                          <u>AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCT</u>
/note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
127 c 165 g 119 t
                                                                                                       32;
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                                                                 Score 300.8; DB 9
Pred. No. 3.6e-81;
0; Mismatches 32
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1. 518
/organism=Homo sapiens"
/isolate="patient CRA"
/db_xref="taxon:9606"
/chromosome="14"
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/gene="VH1-69"
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/gene="VH1-69"
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89.8%;
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Best Local Similarity
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Homo sapiens isolate BRA 1gM heavy chain VH1 region precursor
(VH-69) gene, partial cds.
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Johnson, T.A.
Direct Submission
Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
Jolla, CA 92093, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MDWTWRPLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
GGTFSSYAINWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTNTAYMEL
SSLRSEDTAVYYCARDGCSGGSCYFWGWFDPWGQGTLVTVSS"
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                                                                                         241 TGGAGCTGAGCCGGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
                                                                                                                                                                                                                                                                                                    296 GCGATATITIGACIGGCCTTAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCG 355
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1. (Dases 1 to 518)

1. (Dases 1 to 518)

1. (Dases 1 to 518)

1. Wassenti,L.Z. and Kipps,T.J.

19 VH1 genes expressed in B cell chronic lymphocytic leukemia exhibit distinctive molecular features
J. Immunol. 158 (1), 235-246 (1997)
                                                                                                                                                                                                                                   CCTGCAAGGCTTCTGGAGGCACCTTCAGTATATACTATCAGCTGGGTGCGACAGGCCC
                                CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG
                                                                                                                                        CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
                                                                                                                                                                                                                                                                                301 ATTAIGTTIGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/isolate="patient BRA"
/db xref="taxon:9606"
/chromosome="14"
/map="1492"
/note="CLL: chronic lymphocytic leukemia"
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/gene="VH1-69"
/product="IgM heavy chain VH1 region"
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/gene="VH1-69"
/codon start=1
/product="IgM heavy chain VF
/brotein id="AAC51688.1"
/db_xref="GI:2344916"
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/gene="VH1-69"
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'gene="VH1-69"
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U84161.1 GI:2344915
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Homo sapiens
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HSU84161
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/codon_start=1
/product="Ign heavy chain VH1 region precursor"
/protein_id="AACS1691.1"
/db_xref="d1:2344922"
/translation="MNWTWRPLE-PVAAATGVOSQVQLVQSGAEVKKPGSSVKVSCKAS
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join(1. 46,133. .143)
/gene="VH1-69"
/fgene="VH1-69"
/product="IgM heavy chain VH1 region"
/product="IgM heavy chain VH1 region"
/note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
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                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
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Best Local Similarity 99.8%; Pred. No. 3.66-81;
Matches 336; Conservative 0; Mismatches 32; Indels 6;
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Search completed: July 18, 2003, 13:47:37 Job time : 1032.02 secs

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UI-HF-BKO AGENCOURT 602638543 AGENCOURT UI-HF-BKO UI-HF-BKO UI-HF-BKO UI-HF-BKO UI-HF-BKO AGENCOURT

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Lawaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

El (Bases I to 477)

I (Bases I to 477)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1211 row: n column: 14

High quality sequence stop: 473.

Lication/Qualifiers

11. 477
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AW403940
AW408484
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BQ708868
BM007990
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BQ710011
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COMMENT
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                                                                                                         July 18, 2003, 04:16:54; Search time 637.709 Seconds (without alignments) 9345.860 Million cell updates/sec
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             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                          16154066 segs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
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BG397239 GI:13290687
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 909)

Why-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDN Library Preparation: Ling Hong/Rubin Laboratory

CDN Library Arrayed by: The I. M.A.G. E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.
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TITLE
JOURNAL
COMMENT
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BG397239
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/dorganism="Homo saplens"
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602243363F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4334774 5',
mRNA sequence.
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Eukaryota; Metazoa; 'Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1012)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
http://image.llni.gov
Plate: LLCM1282 row; m column: 03
High quality sequence stop: 848.
Location/Qualifiers
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80.8%; Score 297.4; DB 12;
Best Local Similarity 89.5%; Pred. No. 1.8e-73;
Matches 332; Conservative 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
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/db xref="taxon:9666"

/clone="IMAGE:5301349"

/clone lib="NHH MGC 113"

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ECORI; CDNA made by oligo-dT priming. Directionally cloned
into BCORI/Xho1 sites using the following 5: adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCGTGTATTACTGTGCGAGAGATCCCG 300
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                                                                                                          E Tangers 1 to 359)

S NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLCM2517 row: b column: 06
                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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78.2%; Score 287.8; DB 14; Length 959;
Best Local Similarity 87.9%; Pred. No. 9.5e-71;
Matches 326; Conservative 0; Mismatches 42; Indels 3;
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467 CCGTCTCCTCA 477
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           SOURCE
ORGANISM
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ORIGIN
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: gGACGAGG(6). Size-selected >Sobbp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

Note: this is a NIH MGC Library."
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BQ706226
BQ706226.1 GI:21845125
BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1204 row: m column: 15
High quality sequence stop: 716.
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EST 15-MAY-2001

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/ Organism="Homo saptions"

/ Organism="Homo saptions"

/ Clone="INAGE:4852039"

/ Clone="INAGE:4852039"

/ Clone="INAGE:4852039"

/ Lisue_type="primary B-cells from tonsils (cell line)"

/ Lab. host="DHIOB (phage-resistant)"

/ Note="Organ: B-cells; Vector: pOTB7; Site_1: xhoI;

/ Note="Organ: B-cells; Vector: pOTB7; Site_1: xhoI;

/ Site_2: EcoRI; cDNA made by oligo-dr priming.

Directionally cloned into EcoRI/Xhoi sites using the following 5' adaptor: GGGACGAG(G). Size-selected >500ppfor adaptor: GGCACGAG(G). Size-selected >500ppfor adaptor: GGCACGAG(G). Size-selected by Ling for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH MGC Library. " I others
                                                                                            ICSM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 903)

NIH-MCG http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.inh.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIALL)

Clone distribution: MGC clone distribution information can be thep://image.linh.gov

Plate: LiCMI655 row: n column: 08

High quality sequence stop: 813.

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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCC 299
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602711631F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852039 5', mRNA sequence.
BG754936
EG754936.1 GI:14065589
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Home sapiens

Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RS NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Conteat: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov/.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Runin Laboratory

CDNA Library Preparation: Ling Hong/Runin Laboratory

CDNA Library Preparation: Ling Hong/Runin Laboratory

CDNA Library Preparation: Ling Hong/Runin Laboratory

CDNA Library Preparation: Ling Hong/Runin Laboratory

CLone distribution: MGC clone distribution information can be http://mage.lin.gov

Clone distribution: Stop: 833.

Clone Library Raquence stop: 833.

Location/Qualifiers

1. 878

Location/Qualifiers

1. 878

Location/Qualifiers

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Location/Qualifiers

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Location/Qualifiers

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Location/Qualifiers

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Location/Dubit Berkeles/ Site 1: Xhol;

Alab-host="Bulb Berkeles/ Site 1: Xhol;

Clone lib="Number" Embrary B-cells from tonsils (cell line)"

And Andres Embrary Site 2: Rock: CDNA made by oligo-dT priming:

Andrea Library Cloned into Econify Constructed by Ling Carlifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

MAT 196 a 258 C 246 9 177 t 1 others
602712658F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852934 5',
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/clone_lib="NHH MGC 113"
/lab_host="DH10B" (phage-resistant)"
/lab_host="DH10B" (phage-resistant)"
/note="Corgan: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                            1035 bp mRNA linear EST 16-AUG-2002
_8642770 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6295574
CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGAAGAATCCACGAGCACCAGAGCTACA 341
                                                                                                                                                                 301 ATTATGTTTGGGGGAGGGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                                                                       TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGGAGAGATCCCG 300
                                                                                                    402 ACACACCICCTTGGTTTG---GTGTGTTTGACTACTGGGGCCAGGGAACCCTGGTCACCG 458
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate://image.llnl.gov
Plate://image.llnl.gov
Plate://image.llnl.gov
High quality sequence start: 71
High quality sequence start: 71
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Pred. No. 2.3e-69,
); Mismatches 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:6295574"
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-340 c 276
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Best Local Similarity 87.1%;
Matches 323; Conservative C
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5', mRNA Sequence
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BQ881378
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/lab_host="UPH10B" (phage-resistant)"
/note="Urgan: splean; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG (3). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
MIH MGC Library.

**A 181 t 2 others**
                                                                                                                                                                                                                                                                                                           BQ706171 903 bp mRNA linear EST 16-JUL-2002
AGENCOURT 8354485 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281064
5, mRNA sequence.
BQ706171
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                                                                         385 ATTGTAGTAGTACCAGCTGCTGTACTTTGACTACTGGGGCCA-GGAACCCTGGTCA 443
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325 TGGAGĊTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGAT 384
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Flate: LLCM243 row: e column: 01
High quality sequence stop: 576.
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                                              1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6281064"
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EMEATOCLE; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Futhmates; Catarrhini; Hominidae; Homo.

1 (Dases I to 980)

2 MIH-MGC http://mgc.ncd..nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: Ggapbs r@mail.nih.gov

CDNA Library Preparation: Mubin Laboratory

CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be http://mage.lln.gov. ocolumn: 24

High quality sequence stor: 254.

High quality sequence stor: 254.

High quality sequence stor: 254.

Abordation/Qualifiers

1 0.980

//db.rate="URMAGE:621647"

//clone='INMAGE:621647"

//clone-'INMAGE:621647"

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BQ708591 GI:21847477
                                                                                            240
                     241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
                                                                                                                                                                                                                   404 TGGAGCTGAGCACCCTGAGATCTGAGGACACGGCCGTATATTATTGTGCGGAGAGTGCCC 463
CTGGACAAGGGCTTGAGTGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                                                                                                                                                                                                                  301 ATTATGTTTGG---GGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA
                                                                                    CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAACTACA
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Bukaryota, Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 991)

1 NH-MGC http://mgc.nci.nih.gov/.

1 National Institutes of Health, Mammalian Gene Collection (MGC)

1 Unpublished (1999)

1 Contact: Robert Strausberg, Ph.D.

2 Email: Gapba-remail.nih.gov

1 Tissue Procurement: Dr. Mark Watson

1 Contact: Robert Strausberg, Ph.D.

2 Email: Gapba-remail.nih.gov

1 Tissue Procurement: Dr. Mark Watson

1 Contact: Preparation: Rubin Laboratory

1 Contact: Mark Macson

1 NA.AG.E. Consortium (LLNL)

1 DNA Sequencing by: Agencourt Bioscience Corporation

1 Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at:

1 High quality sequence stop: 587.

1 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGENCORT_7976230 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214702 5', MRNA sequence.
BQ710257 I GI:21849156
EST. human.
Homo sapiens
EVALOR SAPIENS
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                                                                                                                                                                                                                                                                                                                                                                       298 TGGAGTTGAGCCAGCCTGAGATCTGAGGACACGGCCGTGTTTTACTGTGCGAGAGATAACG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTATGITIGGGGGAGCGACAACTGGTICGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 ACTATGAACG-----AATTGGGTTTGACTCCTGGGGCCAGGGAACCCTGGTCACCG 408
58 AGGIGCAGCTGGTGCAGTCTGGGGCTGAAGAAGCCTGGGTCTCGGTGAAGGTCT
                                                                                                       1118 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATACTATCAACTGGGTGCGACAGGCCC
                                                                                                                                                                                        CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                                     181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCTTACA
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AW408371 16-FEB-2000 UI-HF-BK0-abk-c-03-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3056620 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

Clone distribution: M.C. clone distribution information can be
found through the I.M.A.G.E. Consortium/LMN at:

www-bio.lnh.gov/bbrp/image/image.html

Seg primer: M13 Forward.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
           this is
                                                                                                                                                                                                               Gaps
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3
Superscript II RT (Life Technologies). Note:
NIH MGC Library." 3 others
                                                                                                                                                 Length 970,
                                                                                                                                                 Score 279; DB 14; Length 9
Pred. No. 3e-68;
); Mismatches 45; Indels
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/clone lib="NTH MGC_36"
/tissue_type="1ymph"
/cell_type="germinal center B cells"
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AW408371.1 GI:6927428
                                                                                                                                                 75.8%;
86.9%;
                                                                                                                                                   Query Match
Best Local Similarity 86.9
Matches 319; Conservative
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AW408371
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BQ706539.1 GI:21845438
EST.
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/db_xref="taxon.9606"
/clone=lib="NHMGE:630062"
/clone=lib="NHMGE:630062"
/lab_host="DH10B" (phage-resistant)"
/lab_host="DH10B" (phage-resistant)"
/note="Corgan: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
Foots="Corgan: spleen; Vector: potential of the corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; Corgan: spleen; C
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MNH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2515 row: c column: 23
High quality sequence stop: 569.
                                                                 . 9
              DB 14; Length 991;
                                                                 Indels
                                                                    44;
     76.5%; Score 281.6; DB 1.
llarity 86.6%; Pred. No. 5.5e-69;
Conservative 0; Mismatches 44
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: ECORI, CoDAM made by O olgo-dry priming. Directionally cloned into ECORI(XhoI sites using the following 5 dapptor: GCOACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Superscript II RT (Life Technologies). Note: this is a 291 c 246 g 162 t
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Bukaryota, Merazoa; Chordata, Craniata; Vertebrata; Euteleostomi;

Bukaryota, Merazoa; Chordata, Craniata; Vertebrata; Euteleostomi;

Bukaryota, Merazoa; Chordata, Craniata; Vertebrata; Euteleostomi;

I (bases it to 937)

NIH-MGC http://mgc.nci.nih.gov/

Mational Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Straubberg, Ph.D.

Contact: Robert Straubberg, Ph.D.

Tissue Procurement: Dr. Mark Watson

Contact: Robert Strayed by: The I M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be the p://maga.lln.gov/

Plate: LLCM3383 row: i column: 03

High quality sequence stop: 516.

Incention/Qualifiers

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                                                                                                                                                                                                                   Score 277.2; DB 14; Length 884;
Pred. No. 9.1e-68;
0; Mismatches 43; Indels 6;
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                                                                                                                                                                                                                 75.3%;
86.7%;
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Best Local Similarity 86.77
Matches 319, Conservative
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/cell_line="WGC85"
| Alab host="DH10B (LTI)" |
| Alab host="DH10B (LTI)" |
| Alab host="Vector: pT713-Pac; Site_1: Not1; Site_2: Eco RI;
| Constructed from size fractionated cytoplasmic mRNA (0.5-1:Skb). Directionally cloned. Cells provided by Louis Most Standt, Ph.D. Libtrary preparation by Maria de Patima Bonaldo, Ph.D. and M. Benco Soares, Ph.D."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I (bases 1 to 884)

I (bases 1 to 884)

NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)

Clond Attribution: MGC clone distribution information can be http://image.llnl.gov.b. Consortium/LLNL at:

Flate: LLCM2384 row: Column: 24

High quality sequence stop: 631.

Luce

Lucation/Qualifiers

Luce

//remainsm="Homo saniens"
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BQ708380 BQ708380. I GI:21847279
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al Similarity 88.5%; Pred. No. 2.2e-68;
317; Conservative 0; Mismatches 32; Indels 9;
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/db xref="Laxon:9606"
/clone="IMAGE:6215351"
/clone_lib="NATH MGC 113"
/lab_host="DH10B (phage-resistant)"
                                                                                                                          ø
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/note="Vector: pT713-Pac, Site 1: Not1; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Benaddo, Ph.D. and M. Bento Scares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTTTCAGCTGGGTGCGACAGGCCC 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Indels
            at:
                                                                                                                    /organism="Homo sapiens"

/db xref="taxon:9606"

/clone="IMAGE:305339"

/clone lib="NIH MGC 36"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_nost="DH10B (LTI)"
         Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 276.6; DB 10
Pred. No. 9.3e-68;
0; Mismatches 49;
                           www-bio.llnī.gov/bbrp/image/image.htmi
Seg primer: M13 Forward.
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    found through the I.M.A.G.E.
                                                                            Location/Qualifiers
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larity 86.0%;
Conservative (
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/organism="Homo sapiens"

/db xref="taxon:9606"

/clone="IMAGE:621514"

/clone="IMAGE:621514"

/clone="IMAGE:621514"

/clone="IMAGE:621514"

/lab host="DH10B (phage-resistant)"

/lab host="DH40B (phage-resistant)"

/note="Organ: spleen; Vector: pOTB7; Site_1: Xho1; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/Xho1 sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 418)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapberremail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UI-HF-BKO-aad-f-06-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone AW401468
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                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                     75.3%; Score 277.2; DB 14; Length 937; 86.7%; Pred. No. 9.4e-68; ive 0; Mismatches 43; Indels 6;
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Human cancer cell
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Colon adenocarcino
Lung cancer relate
DNA encoding antiHuman anti-factor

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Run on:

Scoring table:

Searched:

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/*tag=
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AAF29080
AAC67868
AAA48411
AAF29714
AAQ22419
AAQ44185
AAT37243
                                                                                                     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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DNA encoding anti-Human FVIII antibo Human secreted pro

91WO-US08605

18-NOV-1991;

G71-1 immunoconjug Human heavy chain Human heavy chain DNA fragment vh49.

354 1517 812 812 812

293.2 293.2 289.6 286.4 286.4 287.8 280.8 280.8

126459786

Score

Result No.

Human LH13 monoclo immunoconjug

11-JUN-1992

Anti-FAPalpha anti Human anti-GPIIb/I

Humanised murine

DNA encoding anti-Anti-human CD154 a Human secreted pro CEA6 antibody sing

DNA encoding anti-CEA-specific antib Antibody D heavy c Human Ig-M heavy c Human cDNA encodin Human cDNA encodin DNA encoding anti-Human cDNA encodin Human cDNA encodin

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The gene (AAT60739) encoding 1gG1 (AAW10550) can be subjected to sit directed mutagenesis in order to introduce one or more N-linked glycan addition sites into the 1gG1 molecule (see also AAW10551). Bukaryotic host cells co-transfected with a vector carrying the the mutated 1gG1 gene and with a vector that expresses an alpha-(1,3) Eucosyltransferase capable of attaching sialyl-Le(x) groups at the glycosylation sites of the antibody molecule can be used in the prodn. of sallyl-Le(x)-modified antibody. Such an antibody has prodn. of sallyl-Le(x)-minimising inflammation and decreasing extravasation-dependent organ damage and/or clotting.
        extravasation-dependent adverse reaction; organ damage; clotting; adult respiratory distress syndrome; glomerular nephritis; ischaemic myocardial injury; immune reaction; septic shock; septicaemia; therapy; diagnosis; ds.
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Pred. No. 5.6e-75;
0; Mismatches 33; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                 P-selectin and opt. E-selectin binding organic mol. - having sialyl-Le(x) and sulphated determinant, useful for protecting against inflammatory or immune reactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 40-41; 81pp; English.
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Best Local Similarity 88.2<sup>s</sup>
Matches 335; Conservative
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P-PSDB; AAW10550.
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                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                        The IgG1, in its nascent form, bears no sialyl-Lex side chains. The inventors designed a molecule including several such sites for attachment of sialyl-Lex side chains (see AAR2442, FT). The additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fr acceptor binding ability. They are preferably located in the CHZ region of the Ig molecule. Antibodies bearing multiple sialyl-Lex determinants are useful for disrupting undesirable interactions between cells or proteins. Bisrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 2287;
                                                                                                                                                               Inhibition of cell adhesion mediated through ELAM-1 mol. bindi
- used in treating chronic inflammation, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IgG1; P-selectin ligand; PSGL-1; counter-receptor; E-selectin;
sialyl-Lewis X; antiinflammatory; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.7%; Score 293.2; DB 13; Length ilarity 88.2%; Pred. No. 5.6e-75; Conservative 0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2287 BP; 483 A; 753 C; 652 G; 399 T; 0 other;
                                                                                                                                                                                                                                       Disclosure; Fig 1; 46pp, English.
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90US-0618314
                                  (GEHO ) GEN HOSPITAL CORP
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P-PSDB; AAR24442.
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Best Local Similarity
Matches 335; Conserv
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23-NOV-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HTV-1) envelope glycoprotein gpl20. These can be used in diagnosis and therapy of HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1 infected mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGGIGCAGCIGGIGCAGICTGGGGCTGAGGTGAAGACCTGGGTCCTCGGTAAAGGICT
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                                                                                                                                                                                                                                                                            Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Indels
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88.0%; Pred. No. 3.9e-74;
iive 0; Mismatches 39
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                                                                                     AAF29080 standard; DNA; 378
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nes 329; Conservative
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P-PSDB; AAB62779.
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                                                                                                                                                                                                              03-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watkins
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CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a recombinant human antibody scFv. Antibody TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope recognised by TN11 is located inside domain C of TN-C. TN11 is therefore only capable of recognising TN-C isoforms containing domain C (cTN-C). TN11 is useful for detecting the presence of TN-C isoforms in vitro or in vivo for diagnosing pathologies expressing the cTN-C isoforms of TN-C. It is useful for the preparation of formulations for the treatment of human neoplasias.
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                                                                                                                                                                                                                                                                                                                                                                                                         Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;
cTN-C; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTGCTGGTGCTGGGGGTGAGGTGAAGGTGAAGCCTGGGTCTCGGTGAAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ligands used for diagnosis and treatment of human neoplasias, are capable of identifying the tenascin-C isoform containing domain {\tt C}
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                                                                                                                                                                                                                                                                                                                                                               Recombinant human antibody scFv TN11 nucleotide sequence.
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Pred. No. 3.9e-73;
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                                                                                                                                                                                           BP.
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86.1%;
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Matches 317; Conservative
355 TCATCGTCTCCTCA
                                                                                                                                                                                           AAC67868 standard; DNA;
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The present sequence encodes the heavy chain variable region of a human tumour-specific monoclonal antibody. Neoplastic cells selectively express antigodies can be produced that are specifically directed against tumour-specific antigens. The antibodies can be conjugated to cytocoxic or cytostatic agents and used to selectively target cancer cells for the confidence or tumours. They can also be linked to diagnostic moieties that allow the imaging of neoplastic cells. Nucleic acids encoding human tumour-specific monoclonal antibodies can be used to express the antibodies with higher affinity or higher selectivity for tumour cells. The nucleic appearance of produced modified antibodies with higher affinity or higher selectivity for tumour cells. The nucleic acids encoding the presented by in vitro immunisation of human spleen cell cultures with breast carcinoma cells. The nucleic acid encoding the monoclonal antibody exact then isolated from the hybridoma by RT-PCR. The present sequence mocodes a human monoclonal antibody encoding the more assumed by LHI3 hybridoma cell line.
ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGGCCAGGGAACCCTGCTCATCG 360
                                                                                 GTATTACGATTTTTGGAGGAGGTGCTTTCGATATCTGGGGCCGAGGCACCATGGTCACCG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New tumor-specific human monoclonal antibody, useful for the treatment and diagnosis of cancer, comprises at least one complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "LH13 antibody heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                      Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cancer; cytostatic; cytotoxic; heavy chain variable region; ss.
                                                                                                                                                                                                                                                                                                                      Human LH13 monoclonal antibody heavy chain variable region cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 82; 84pp; English.
                                                                                                                                                                                                                           AAA48411 standard; cDNA; 354 BP.
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/prc²
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/*tag=
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                                                                                                                                                 rcrcrrca 369
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P-PSDB; AAY99558.
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                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Sequence 354 BP; 80 A; 90 C; 115 G; 69 T; 0 other;

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CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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                                                                                                                                                                                                                                                                       182 CACAGAAGTICCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241
                                                                                                                                                                                                                                                                                                       241 TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
                                                                                                                                                                                                                                                                                                                              242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGA----- 296
                                                                                                                                                                                                                                                                                                                                                                                             -----AGATAGCAGTGGCTGGTATCACTACTGGGGCCAGGGAACCCTGGTCACCG
                                                                9
                                                                                                                                                                                                                                                                                                                                                                  301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a composition comprising a homodimeric immunoconjugate protein made up of two chains, each containing an 1gG1 Fc effector domain and a targeting domain. The targeting domain may be
                                                                                           19
                                                                                                                                                                               121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG
                                                           1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAGCCTGGGTCCTCGGTAAAAGGTCT
                                                                                       2 AGGTGCAGCTGCAGTCTGGGGCTGAGGTGAAGAGCCTGGGTCCTCGGTGAAGGTCT
                                                                                                                                                  62 ccrecaagecricigaagecaccricageagecrarecrareacrigacigegacagecec
                                                                                                                                                                                                            122 Crágacaadagacrigagragaragagagagarcarccrarcriragracaacaaacraca
                                                                                                                                                                                                                                          181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoconjugate protein for treatment of neovascularization, comprises protein comprising Fc region of human immunoglobulin (1g)GI conjugated to the targeting domain which comprises factor VII mutant -
                                  Gaps
                                  15;
Score 284.8; DB 21; Length 354;
Pred. No. 9.5e-73;
); Mismatches 27; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse, scPv, immunoconjugate, IgG1 effector domain, catherosclerosis, tissue factor; macular degeneration; rheumatoid arthritis, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G71-1 immunoconjugate coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 65-66; 69pp; English.
                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF29714 standard; DNA; 1517 BP
Query Match 77.4%;
Best Local Similarity 88.6%;
Matches 326; Conservative
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WPI; 1992-113962/14.
P-PSDB; AAR22358.
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                       28-AUG-1991;
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                                        31-AUG-1990;
29-AUG-1990;
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      19-MAR-1992
                                                                                    Lonberg N,
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either the human IgG1 Fc region or a mutant form of human factor VII. The immunoconjugate is targeted at the transmembrane receptor tissue factor. This enables the composition to be used in the treatment of diseases associated with neovascularisation, including cancer, atherosclerosis,
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                                                                                                                                                CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
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                                                                                              Gaps
                                                                                            12;
                                                                                                                                                                                                                                                                           TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA
                                                                          DB 22; Length
                                                                                            32; Indels
                                                        Sequence 1517 BP; 338 A; 444 C; 441 G; 294 T; 0 other;
                                                                         Score 282.8; DB 2
Pred. No. 5.2e-72;
); Mismatches 32
                                         rheumatoid arthritis and macular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signal"
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note= "recombination signal"
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/note= "recombination
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88.0%;
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287..373
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373..812
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241..689
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678..686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector lambda FIX II was screened with the human VH1 family specific oligonucleotide (see AAQ22418). Phage clone lambda 49.8 was isolated and a 6.1 k Xbal fragment contg. the variable segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8 An 800 bp region of this insert was sequenced. VH49.8 was found to have an open reading frame and intect splicing and recombination seignals, thus indicating that the gene is functional.
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non-rearranged and/or rearranged Ig chains
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0; Mismatches 12;
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isotype switching; H chain variable region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human heavy chain V region gene VH49.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 14; Page 87; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.3%;
96.0%;
                                                                                                                90US-0575962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ44185 standard; DNA; 812
91WO-US06185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 96.0
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                (GENP-) GENPHARM INT INC
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CTGGACAAGGCTTGAGTGGATGGGAACGATCATCCTTGGACTAGCAATTACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGCGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGGIGCAGCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 AGGICCAGCIGCAGICIGGGCIGAGGIGAAGAAGCCIGGGICCICGGIGAAGGICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the variable heavy chain gene segment containing human DNA fragment, vh49.8 which was injected into half day mouse embryo pronuclei, to generate an unrearranged heavy chain minilocus transgene. The resulting transgenic mice can be used for the production of heterologous (i.e. human) antibodies against specific antigens, this comprises immunising a mouse with a preselected antigen and collecting antigen binding heterologous
                                                                                                                                                                                        Variable; heavy chain; gene segment; human; DNA fragment; vh49.8; unrearranged; minilocus; transgene; transgenic; mouse; production; heterologous; antibody; gamma; immunoglobulin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.3%; Score 280.8; DB 17; Length 812; 96.0%; Pred; No. 1.7e-71; ive 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of heterologous human immunoglobulin(s) - by immunising
                                                                                                                                                       DNA fragment vh49.8, containing variable heavy chain gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 12; Columns 61-62; 94pp; English.
                                                                                                                                                                                                                                                                                              Location/Qualifiers
241.286
/*tag= a
373.437
/*tag= b
                                                              ВЪ
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90US-0574748.
90US-0575962.
91US-0813279.
92US-0853408.
                                                          AAT37243 standard; DNA; 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.3
Best Local Similarity 96.0
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENP-) GENPHARM INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-383736/38.
P-PSDB; AAW03950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay RM, Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1992;
29-AUG-1990;
31-AUG-1990;
17-DEC-1991;
18-MAR-1992;
23-JUN-1992;
                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                            21-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                               US5545806-A.
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                                                                                           AAT37243;
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                           RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 AGGTCCAGCTGGTGCAGTCTGGGGGTGAGGTGAAGCCTGGGTCTGGGTCTGGTGTT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGACAAGGGCTTGAGTGGATGGATCATCCTTTCTTTGTTGCAAACTACG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGAACAAATCCACGAGCACAAGCTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A human placental genomic DNA library cloned into the phage vector lambda FIX II was soreened with the human VH1 family specific oligonucleotide AAQ44184. Phage clone lambda 49.8 was isolated and 6.1kb Xbal fragment containing the variable segment W449.8 was subcloned into pNNO3 to generate plasmid pVH49.8. An 800bp region of this insert was sequenced (AAQ44185) and VH49.8 found to have an open reading frame and intact splicing and recombination signals, indicating that the gene is functional.
/*tag= a / number= 1 287.372 / *tag= b / number= 1 373.812 c / number= 2 241.689 / *tag= c / number= 2 241.689 / *tag= (DS is interrupted by intron #1; the translated in the amino acid sequence AAR38623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic non-human animals contg. immunoglobulin heavy chain trans gene - used to produce useful antibodies by isotype switching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.3%; Score 280.8; DB 14; Length 812; Best Local Similarity 96.0%; Pred. No. 1.7e-71; Matches 288; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 12; Page 96; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                91US-0810279.
92US-0853408.
92US-0904068.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-214169/26.
P-PSDB; AAR38623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kay RM, Lonberg N;
                                                                                                                                                                                                                                                                                                                                                17-DEC-1991;
18-MAR-1992;
23-JUN-1992;
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switching in lymphocytes
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                                                                                                                                                   Transgenic mouse; human; immunoglobulin; heavy chain segment; J region; joining region; constant region; VH family; variable gene; gamma isotype; diversity gene; isotype switching sequence; mu isotype; Ig production; monoclonal antibody; MAD production; antigen; heavy chain isotype;
                             624
                                        CTGGACAAGGGCTTGAGTGGATGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564
                     CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human antibody producing transgenic mouse - containing transgene comprising human V, D and J genes and sequences to provide isotype
                                                                                                                                                                                                                          /*tag= a
/note= "contains an intron, no stop codon given"
                                                                                                                                                                                                           Location/Qualifiers
241..678
                                                                                          AAV12538 standard; DNA; 812 BP
                                                                                                                                                                                                                                                                                                                                                       94US-0352322.
90US-0574748.
90US-0875962.
91US-0810279.
92US-0853408.
92US-099086.
92US-0990860.
93US-0953131.
                                                                                                                                     Human VHI family gene VH49.8.
                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0155301.
93US-0161739.
93US-0165699.
                                                                                                                                                                                                                                                                                                                                           94US-0352322
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                                                                                                                                                                                                                                                                           /number= 1
373..678
/*tag= d
/number= 2
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                       number= 1
                                                                                                                                                                                antigenic stimulation; ss.
                                                                                                                                                                                                                                               *tag= b
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                                                                                                                                                                                                                                                              287..372
/*tag= c
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                                                                                                                                                                                                                                         241..286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kay RM, Lonberg N;
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P-PSDB; AAW41113
                                                                                                                                                                                              Homo sapiens
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                                                                                                                       26-MAY-1998
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17-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-1992
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               181
                                                                                                         AAV12538;
                                                                                                                                                                                                                                         exon
                                                                            RESULT 10
                                                                                    AAV12538
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contains in its genome a transgence comprising in operable linkage human variable (V), diversity (D) and junction (J) genes, a human mu constant region gene (muCH), at least 2 different non-um human CH genes and secondated isotype switching sequences, where human mu and gamma switch sequences are located in closer proximity to each other than in the naturally occurring human immunoglobulin (Ig) locus, and where in lymphocytes of the mouse the transgene undergoes productive VbJ rearrangement and gamma sequences, so that the mouse product se serum the human mu and gamma sequences, so that the mouse produces a serum the human mu and gamma sequences, so that the mouse produce human to antigenic stimulation. The transgene can be used to produce human Ig and monoclonal antibodies (WAb), which are specifically reactive with human antigens. The MAD can be used in therapeutic or diagnostic applications. The transgenic mice can produce human MAb of multiple isotypes by undergoing isotype switching.
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                                                         This sequence represents the human VHI family gene VH49.8. This DNA sequence can be used in a plasmid, which is used to develop the transgenic mouse of the invention. The transgenic mouse of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 280.8; DB 18; Length
Pred. No. 1.7e-71;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "heavy chain V region gene"
287..372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunoglobulin VH1 family VH49-8 gene.
Example 12; Column 73-74; 153pp; English.
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/product= VH49.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT70522 standard; DNA; 812 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.09
Watches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241..677
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/*tag= c
/number= 2
/note= "Whe protein shown in the specification ends at
position 677, not at the stop codon ending at
position 689"
                                                                                                                                                        'DNA sequence in the specification is unclear, so this is the best estimate of the sequence"
          Ig; affinity constant; human; antigen; hybridoma; B cell; t. transgenic; mouse; CD4; antibody; autoimmune; inflammatory; transplant rejection; immunoglobulin; ss.
                                                                            Location/Qualifiers
241..286
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/anticodon= 1
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P-PSDB; AAW24777.
                                                                                                                                                                                                                                                                                                                                                             Lonberg
                                                     Homo sapiens
                                                                                                                                                                                                                                                                                             10-OCT-1996;
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                                                                                        exon
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                                                                          Key
          %XCCCCCCCCCCCCX8Xx14X2BBX1X3X4X5AXBXX14414141414141414448X8X44X8
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                                                                                                                                                                                                                                                                                                     This sequence encodes the VH49.8 gene from the human heavy chain V region and a member of the VH1 family. This gene was sequenced from the plasmid pVH49.8 which is used in a novel method of developing transgenic non-human animals capable of producing heterologous antibodies encoded by human immunoglobulin genes. Such transgenically produced monoclonal antibodies should alleviate the intrinsic immunogenicity of non-human immunoglobulins allowing the development of new in vivo applications.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 AGGICCAGCIGCAGTCTCGGGCTCAGGGAAAAAGCCIGGGICCICGGIGAAAGGICT 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATGGACTAGCAAATTACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 CIGGACAAGGGCIIGAGGGAIGGAAGGATCATCCCIAICCIIGGTAIAGCAAACIACG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                  Transgenic mouse for heterologous antibody production - containing DNA encoding human immunoglobulin components
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.3%; Score 280.8; DB 18; Length 812; Best Local Similarity 96.0%; Pred. No. 1.7e-71; Matches 288; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
680..684
//ttag= c
70ttag= mentioned in specification"
710..718
                                    710..718
/*tag= d
/note= "Mentioned in specification"
                                                                                                                                                                                                                                                                                   Example 14; Column 54; 90pp; English
                                                                                                                                          90US-0574448.
                                                                                                                        92US-0834539
                                                                                                                                                                                                                    WPI; 1997-297410/27.
N-PSDB; AAW18840; AAW18841.
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                                                                                                                                                                         (GENP-) GENPHARM INT INC.
                                                                                                                                                                                                Lonberg N;
  misc_feature
                                 misc_feature
                                                                                                                    05-FEB-1992;
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                                                                          US5633425-A
                                                                                              27-MAY-1997
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                                                                                                         A novel composition has been developed which comprises an immunoglobulin [19] having an affinity constant (Ka) of at least 2 multiply 10000000000 M-1 for binding to a predetermined human antigen. The present sequence represents the human 1019 of solated from a human placental genomic library lambda. Anti-CD4 antibodies from may be used in therapeutic and diagnostic applications, especially activity of CD4 cells and reduce undesirable autoimmune reactions, inflammatory response and renaplant rejection. Transgenic animals are tangebale of producing heterologous antibodies of multiple isotypes by its necessary for antigen-stimulated B-cell maturation and can switch to encode and produce one or more subsequent heterologous isotypes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 ccidcaadgcircigaaggcaccircagcaacraigaricagciaggracaacaaggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGACAAGGGCTTGAGTGGATGGAAGGATCATGCCTATGGACTAGCAAATTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Novel anti-CD4 antibody produced by transgenic mice - used in the treatment of auto-immune disease etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18; Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 280.8; DB 18; Length
Pred. No. 1.7e-71;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 812 BP; 203 A; 194 C; 223 G; 192 T; 0 other;
                                                                       Example 12; Page 138; 396pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.3%; Sco
Best Local Similarity 96.0%; Pre
Matches 288; Conservative 0;
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Human VH1 gene VH49.8.

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                 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA
                                                                TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG
                                                                                                                                                                                                                                                                                                                                  transgenic mouse; human heavy chain transgene; digoxin; human light chain transgene; immortalized cell; immunoglobulin; Shinga-like toxin; autoimmune disease; cancer; infectious disease; transplant rejection; blood disorder; coaqulation disorder; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents human heavy chain V region gene VH49.8, which is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel transgenic non-human animals used to produce heterologous
                                                                                                                                                                                                                                                                                  Nucleotide sequence of human heavy chain V region gene VH49.8.
                                                                                                                                                                                                                                                                                                                  Transgenic animal; heterologous antibody; hybridoma; B cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 812 BP; 204 A; 188 C; 223 G; 196 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 12; Page 168; 484pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ball WJ;
                                                                                                                                                                                  BP.
                                                                                                                                                                                AAZ21897 standard; DNA; 812
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                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9945962-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1999;
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                                                                                                                                                                                                                                                 24-NOV-1999
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                               504
                                                                180
                                                                                               564
                                                                                                                                240
                                                                                                                                                                 624
                                                                                                                                                                                                                     TGGAGCTGAGCCTGAGATCTGAGGACACGCCGTGTATTACTGTGCGAGAGACACAG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, Immunoglobulin transgene, Ig; VH gene; D gene, JH gene; mu gene; switch sequence; gamma gene; IgM; IgG; ss.
                                                                                                                                                     CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACCAGCCTACA
                                                                                                                                                                                                  TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG
                                445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC
                                                                                               CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCTACA
CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
                                                                CTGGACAAGGGCTTGAGTGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a heavy chain (human) immunoglobulin (Ig) transgene. The transgene comprises: (i) human VH gene segments; (ii) human D gene segments; (iii) human JH gene segments; and either (iv) amu constant region comprising a mu switch sequence upstream from a mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunoglobulin transgene - with mu and gamma isotype switching
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of human VH1 family gene VH 49.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 14; Column 53-54; 88pp; English.
                                                                                                                                                                                                                                                                                                                  BP
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90US-0574748.
90US-0575962.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS5874299-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-FEB-1992
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                                                                                                                                                                 565
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                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                   AAX06042;
                                                                                                                                                                                                                                   625
61
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Gaps

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12; Indels

1.7e-71

· 0; Mismatches 76.3%; Score 280.8; 96.0%; Pred. No. 1.70

Matches 288; Conservative

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Local Similarity

Query Match

DB 20; Length 812;

9

385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAAGAAGAAGCCTGGGTCCTCGGTAAAGGTCT

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444
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animals to produce heterologous (human) Ig's with varying specificities. The presence of mu and gamma switch segments allows isotype switching of the human heavy chain mini-locus from IgM (for maturation) to IgG.
                                                                                                                                                                                                                                                                          1 AGGTGCAGCTGGTGCAGTCTGGGGGTGAAGAAGAAGCCTGGGTCCTCGGTAAAGGTCT
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin shagements were obtained. 13/15 clones of H chain (IGG1) genes showed homology to the closest germline genes, DP10 (AAQ89327) and HV1263 (AAQ89328). The DNA (AAQ89329) and corresp. amino acid (AAR72070), sequences of the VH region of a representative clone,
                                                                                                                                                                                                                                       ۰,

    produced

                                                                                                                                                                 Query Match 76.3%; Score 280.8; DB 20; Length 912; Best Local Similarity 96.0%; Pred. No. 1.7e-71; Matches 288; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; VH; autoimmunity; ss.
                                                                                                               Sequence '812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aves' ophthalmopathy-associated monoclonal antibody molecular cloning of immunoglobulin genes by PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 68; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NICH-) NICHOLS INST DIAGNOSTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ89328 standard; DNA; 294 BP
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P-PSDB; AAR72069.
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                             94 G; 57 T; 0 other;
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Job time : 96.4001 secs
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1: /cgn2_6/ptodata/1/pubpna/PCT_RBW_PUB.seq:*

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13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1439767 seqs, 1031500376 residues
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368
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			Description	Sequence 92, Appl	Sequence 92, Appl	6	Sequence 19, Appl	Sequence 789, App	Sequence 1604, Ap	Sequence 61, Appl	Sequence 46, Appl	3, 7	ä	Sequence 12, Appl	Sequence 22, Appl	11,	Sequence 7, Appli	Sequence 5, Appli	Sequence 13, Appl
SUMMARIES			ΩI	US-09-925-299-92	US-09-925-299-92	US-10-151-882-9	US-10-091-300-19	US-09-954-456-789	US-09-954-456-1604	US-10-047-542-61	US-10-047-542-46	US-10-151-882-3	US-10-151-882-10	US-09-811-737-12	US-09-811-737-22	US-10-151-882-11	US-10-151-882-7	US-10-151-882-5	US-09-811-737-13
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10 US-09-811-737-21 15 US-10-066-593-54 16 US-08-844-215-24 17 US-08-844-215-27 18 US-08-844-215-27 19 US-08-828-708-12 10 US-09-828-708-12 11 US-09-828-708-12 12 US-09-905-24-8 13 US-09-905-24-8 14 US-09-905-24-8 15 US-10-10-29-70-2 15 US-10-29-70-2 15 US-10-29-70-2 15 US-10-29-70-2 15 US-10-29-70-2 16 US-09-82-29-277 17 US-09-82-29-277 18 US-09-82-29-277 19 US-09-82-29-277 10 US-09-82-29-277 11 US-09-82-29-277 12 US-09-82-29-277 13 US-09-82-29-277 14 US-09-82-29-277 15 US-09-82-29-277 16 US-09-82-29-277 17 US-09-82-29-277 18 US-09-82-29-277 19 US-09-82-29-277 10 US-09-83-18-88-10 11 US-09-83-18-88-10 12 US-09-75-14-88-88-10 13 US-10-16-28-28-10 14 US-09-75-14-88-88-10 15 US-10-18-84-53	ALIGNMENTS 19925299 Acids, Proteins and US/09/925,299 18-10 17/US00/05883 18-10 17/124,270 12 13, or c 18-10 19-	GAGGTGAA GAGGTGAA
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US-10-091-300-19

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US-10-091-300-19

Sequence 19, Application US/10091300

Publication No. US20030108545a1

GENERAL INFORMATION:

APPLICANT: Rockwell, Patricia

APPLICANT: Rockwell, Patricia

APPLICANT: Goldstein, Neil I

TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular

TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist

FILE REFERENCE: 11245/46211

CURRENT APPLICATION WHERE: US/10/091,300

CURRENT FILING DATE: 2002-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCAAGAGATC--- 298
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US-10-151-882-9

Sequence 9, Application US/10151882

Sequence 9. Application US/20030059862A1

Publicantion No. US20030059862A1

APPLICANT Ruben, Steven M.

TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

FILE REFERENCE: PF554

CURRENT APPLICATION NUMBER: US/10/151,882

PRIOR RILING DATE: 2002-05-22

PRIOR RAPLICATION NUMBER: 60/293,100

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 48

SSOTWARE: Patentin version 3.0

LENGTH: 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: DNA encoding A010D09 scFv US-10-151-882-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                      485 GTCACCGTCTC 495
                                354 CICATCGICTC 364
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                                                                                                                                                                                                                                 365 TGGAGCTGAGCCTGAGATCTGAGGACACGGCCATNTATTACTGTGCGARAAGKCCCT 424
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                                                                                                                       CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACACACCTACA 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 92, Application US/09925299
| Publication No. US20030040617A9
| Publication No. US20030040617A9
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PAIO2
| CURRENT APPLICATION NUMBER: US/09/925,299
| CURRENT FILING DATE: 2001-08-10
| PRIOR FILING DATE: 2000-03-08
| PRIOR PILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1556
| SOFTWARE: Patentin Ver. 2:0
| SEQ ID NO 92
| LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.4%; Score 277.6; DB 12, Length Best Local Similarity 85.7%; Pred. No. 3.3e-84; Matches 318; Conservative 3; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
SGANLEM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
COCATION: (402)
COCHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                     354 CTCATCGTCTC 364
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US-09-925-299-92
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121 180

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TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

FILE REPERENCE: 68220-76

CURRENT APPLICATION NUMBER: US/09/954,456

CURRENT APPLICATION NUMBER: US/60/234,052

PRIOR PAPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR PELING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-25

PRIOR PELING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

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PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAGCTGATCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGACAGATCGCT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 ACAGGCAGGCAAATTTTGACCGGGCCCGGGTTGGCTGGTTCGACCCCTGGGGCCAGGCA 452
                                                                                                                                                                                                                                                                                                                                                                                                          152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIGGACAAGGGCIIGAGIGGAIGGGAGGGAICAICCCICITITIGGIACACCAACCIACT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATC--- 297
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                                                                                                                                                                                                                                                                                                                                                                                                          93 AGATGCAGGTGCAGTCTGGGGCTGAAGTAAAGAAGCCTGGGTCCTCGGTGACGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                                                                                                                                                                                1 AGGTGCAGCTGCTGCAGTCTGGGGCTGAGGAGAGCCTGGGTCCTCGGTAAAGGTCT
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                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                       Length 1599;
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                                                                                                                                                                                                                   Score 274; DB 11;
Pred. No. 7.5e-83;
0; Mismatches 45;
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Patent No. US20020115057A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453 CCCTGGTCACCGTCTCTCA 472
                                                                                                                                                                                                                   74.5%;
nilarity 85.0%;
Conservative 0
   ; SCFTWARE: PatentIn version 3.0
; SEQ ID NO 789
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-789
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APPLICANT: Young, Paul
                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 323; Conserv
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TITLE OF INVENTION: Seets

TITLE OF INVENTION: Seets

CURRENT APPLICATION NUMBER: US/09/954,456

CURRENT APPLICATION NUMBER: US/00/233,617

PRIOR PELING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/235,134

PRIOR PLING DATE: 2000-09-25

PRIOR PELING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

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PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,710

PRIOR APPLICATION NUMBER: US/60/235,720

PRIOR APPLICATION NUMBER: US/60/235,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGACAAGGCTTGAGTGGATGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA-----G 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 TGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGAATACG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 ATTACTATGATAGTAGTGGCGTGGCTTCCCCCTTTGACTACTGGGGCCAGGGAACCCTGG 361
                                                                                                                                                                                                                                                                                                                                                                          1 AGGTGCAGCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGICCAGCIGGIGCAGICIGGGGCTGAGGIGAAGAGCCIGGGGCCICAGIGAAGGICI 61
                                                                                                                                                                                                                                                                                                                    Gaps
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9
                                                                                                                                                                                                                                                       Length 375;
                                                                                                                                                                                                                                                                                                                45; Indels
                                                                                                                                                                                                                                                   Score 276; DB 15;
Pred. No. 1.1e-83;
                                                                                                                                                                                                                                                                                                             0; Mismatches
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FILING DATE: 2000-09-27
PAPLICATION NUMBER: US/60/235,840
FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,863
FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 85
SOFTWAREN WordPerfect 8.0 for Windows
SEQ ID NO 19
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 789, Application US/09954456 Patent No. US20020115057A1
                                                                                                                                                                                                                                                   75.0%;
86.2%;
                                                                                                                                                                                                                                                                                                             Matches 319; Conservative
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                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-10-091-300-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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NUMBER
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US SEQUENCE 46, Application US/10047542

SEQUENCE 46, Application NO. US2020168367A1

SEDIAGON US US2020168367A1

SERBEAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: NOVER: 2001-01-26

FILE REFERENCE: 030905.0004.CTF1

CURRENT FILING DATE: 2001-04-28

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,298

NUMBER OF SEQ ID NOS: 101

SOFTWARE: PATENTING VOS: 101

SOFTWARE: PATENTING VOS: 201

LENGTH: 213

TYPE: NA
ORGANISM: Homo sapiens

US-10-047-542-46
                                                                                                                                           CACAGAAGTICCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGACGAATCCACGAGCACAGCCTACA 370
     CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 178
                                                                                                                                                                                        239 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 CTGGACAAGGGCTTGAGTGGGATGGGGGGGTCATCCTATCTTTGGTACAGCAACTACG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGGACAAATCCACGAGGACACGTACA 240
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; Sequence 3, Application US/10151882
; Sequence 4, Application US/10151882
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL); CURRENT APPLICATION NUMBER: US/10/151,882
                                                                                             CTGGACAAGGGCTTGAGTGGATGGAAGGGATCATCCTATCTTTGGTACAGCAAACTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
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Pred. No. 3.4e-82;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 74.0%;
Best Local Similarity 95.6%;
Matches 280; Conservative
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WESTLONGE 61. Application US/10047542

Sequence 61. Application US/10047542

Bublication No. US20020168367A1

GENERAL INFORMATION:

APPLICANT: LARRICK, JAMES W.

APPLICANT: WYCOFF, KEITH L.

TITLE OF INVENTION: NOVEL IMMINOADHESINS FOR TREATING AND PREVENTING VIRAL

TITLE OF INVENTION: NOVEL IMMINOADHESINS FOR TREATING AND PREVENTING VIRAL

TITLE OF INVENTION: ADD BACTFRIAL DISEASES

TITLE OF INVENTION: ADD BACTFRIAL DISEASES

CURRENT APPLICATION NUMBER: US/10/047,542

PRIOR PELLOATION NUMBER: PCF/US01/13932

PRIOR PELLOATION NUMBER: 60/200,298

PRIOR PELLOATION NUMBER: 60/200,298

PRIOR PELLOATION NUMBER: 60/200,428

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

LENGTH: 1884

TYPE: DNA

TYPE: DNA

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                152
                                                                                                                                                                                                                                                                                                                        61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTATATACTATCAGCTGGGTGCGACAGGCCC 120
                                                                                                                                                                                                                                                                                                                                                                   153 CCTGCAAGGCATCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGCGACAGGCCC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGAGAGCCTGGGTCCTCGGTGAAGGTCT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTATATACTATCAGCTGGGTGCGACAGGCCC 120
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Query Match

74.0%; Score 272.2; DB 15; Length 1884;
Best Local Similarity 95.6%; Pred. No. 3.2e-28;
Matches 280; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                              Length 1599;
                                                                                                                                           Score 274; DB 11;
Pred. No. 7.5e-83;
0; Mismatches 45;
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                                                                                                                                           Query Match 74.5%;
Best Local Similarity 85.0%;
Matches 323; Conservative
; SEQ ID NO 1604
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1604
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  CTGGACAAGGGCTTGAGTGGATGGAAGGATCATCCCTATCTTTGGTACAGCAACTACG 181
                                                                                                                                                                     241 TGGAGCTGAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAATCCCG 300
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                                                                                                        CACAGAAGTICCAGGGCAGAGTCACGATTACCGGGGACGAAGTCCCACGAGCCACAGCCTACA
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84.1%; Pred. No. 4.3e-80;
tive ° 0; Mismatches 56; Indels 3;
                                                                                                                                                                                                                  242 regadereadecerceadarereadacacecererarracrerea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09811737
Patent No. US20020099180A1
GENERAL INFORMATION:
APPLICAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 1-1129
FILE REFERENCE: 2001-03-19
CURRENT FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEFT 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Description of Artificial Sequence:
, OTHER INFORMATION: Humanised Antibody
US-09-811-737-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Matches 312; Conservative
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LENGTH: 396
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Sequence 10, Application US/10151882

Sequence 10, Application US/10151882

Publication No. US20030059862A1

GENERAL INFORMATION:
TITLE OF INVENTYON: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

FILE REFERENCE: PF5.4

CURRENT APPLICATION NUMBER: US/10/151,882

CURRENT APPLICATION NUMBER: 60/293,100

PRIOR APPLICATION NUMBER: 60/293,100

PRIOR PILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin Version 3.0

LENGTH: 720
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                                                                                                                                                                                                                                                                                                              72.8%; Score 268; DB 15; Length 735; 94.9%; Pred. No. 6.6e-81; ive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.7%; Score 267.6; DB 15; Length Best Local Similarity 85.9%; Pred. No. 9e-81; Matches 316; Conservative 0; Mismatches 34; Indels
                                                                                                                                                                                                                       ; OTHER INFORMATION: DNA encoding A004G02 scFv
US-10-151-882-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: DNA encoding A027B01 scFv
US-10-151-882-10
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 3
                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Matches 277; Conservative
                                                                                                                                               LENGTH: 735
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CACAGAAAGTICCAGGGCAGAGICACGAITACCGCGGACAAATCCACGAGCACAGCCTACA 240
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US-10-151-882-11

US-10-151-882-11

Sequence 11, Application US/10151882

Publication No. US20030059862A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)

FILE REFRENCE: PF554

CURRENT APPLICATION NUMBER: US/10/151,882

CURRENT FILING DATE: 2002-05-22

PRIOR APPLICATION NUMBER: 60/293,100

NUMBER &F SEQ ID NOS: 48

SOFTWARE: Patentin version 3.0

LENGTH: 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 72 1%; Score 265.4; DB 10; Length 782; Bert Local Similarity 84.1%; Pred. No. 5.2e-80; Matches 312; Conservative 0; Mismatches 56; Indels 3;
RESULT 12
US-09-811-737-22
Sequence 22, Application US/09811737
Sequence 22, Application US/09811737
Sequence 22, Application US/09811737
Sequence 22, Application US/09811737
Sequence 22, Application US/09811737
TITLE OF INVENTION* Human FAP-alpha-specific antibodies
FILE REFERENCE: 1-1129
CURRENT FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
TAVET: NAS.
                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Humanised Antibody
US-09-811-37-27-8
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Publication No. US20030059862A1
Publication No. US20030059862A1
GENERAL INFORMATION
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SEQ ID NOS: 48
SEQ ID NOS: 48
SEQ ID NOS: 48
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                                                                   Query Match
Best Local Similarity 93.5%; Pred. No. 2.1e-79;
Matches 275; Conservative 0; Mismatches 19; Indels 0;
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FEATURE:
OTHER INFORMATION: DNA encoding A053H04 scFv
US-10-151-882-7
; FEATURE:
- OTHER INFORMATION: DNA encoding A027H08 scFv
US-L0-151-882-11
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US-10-151-882-7
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RESULT 15
US-10-151-882-5
is Sequence 5, Application US/10151882
is Sequence 5, Application No. US20030059862A1
is GENERAL INFORMATION:
is APPLICANT: Ruben, Steven M.
is TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
is FILE REFERENCE: PFS54
is CURRENT APPLICATION NUMBER: US/10/151,882
is CURRENT FILING DATE: 2002-05-22
is PRIOR FILING DATE: 2001-05-24
is NUMBER OF SEQ ID NOS: 48
is SOFTWARE: PatentIn version 3.0
is SEQ ID NO 5
is LENGTH: 744
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242 IGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCGAGAG 295
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71.4%; Score 262.8; DB 15; Length 744;
Best Local Similarity 85.2%; Pred. No. 3.9e-79;
Matches 310; Conservative 0; Mismatches 42; Indels 12;
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ORGANISM: Artificial Sequence
FEATURE:
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368
1 aggtgcagctggtgcagtct......ccctgctcatcgtctcctca 368
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Sequence 53
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Patent No. 5723583
GENERAL INFORMATION:
TITLE OF INVENTION: INHIBITION OF CELL ADHESION
TITLE OF INVENTION: INTERACTIONS
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: DASSECTIONS OF THE STATE: DASSECTION OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE 
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88.2%; Pred. No. 7.4e-83;
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                                                                            US-08-264-093-1
US-08-545-099A-8
US-08-545-099A-18
US-08-745-099A-46
US-09-042-353-146
US-08-749-67-26
US-08-749-67-26
US-08-482-882-85
US-08-483-389-85
US-08-483-389-85
US-08-473-503-85
US-08-473-503-85
US-08-473-503-85
US-08-473-503-85
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US-08-473-503-85
US-08-714-017-85
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APPLICATION NUMBER: US/07/618,314C
FILING DATE: No. 572383ember 23, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/067001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Best Local Similarity 88.29
Matches 335; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
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121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCÀAATTACG 180
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   Pred. No. 7.4e-83;
0; Mismatches 33; Indels
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GITY: Boston
STATE: 225 FrankIn Street
GITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER: Bashable FORM:
MEDIUM TYPE: 3.5. Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM PC. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
FLIGH DATE: 05 June 1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US/08/462,571
FLING DATE: 23 No. 5858983ember 1990
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 35,238
REFERENCE/OCKET NUMBER: 35,238
REFERENCE/OCKET NUMBER: 00786/067002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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      88.2%;
Best Local Similarity 88.2
Matches 335, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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STRANDEDNESS: single
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TITLE OF INVENTION: INHIBITION OF CELL ADHESION
TITLE OF INVENTION: INHIBITION OF CELL ADHESION
TITLE OF INVENTION: INHIBITION OF CELL ADHESION
TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
NUMBER OF SEQUENCES: SCORRESSOR OF COUNTY.
TITLE OF INVENTION EADHERSS:
ADDRESSEE: 125 Franklin Street
CITY: BOSCON
STREET: 225 Franklin Street
COUNTY: USA
ZIP: MA
COUNTY: USA
ZIP: 0210-2804
COUNTY: USA
ZIP: O210-2804
COUNTY: ISM PC Compatible
COMPUTER: READABLE FORM:
MEDIUT TYPE: PLORPY disk
COMPUTER: EMP PC Compatible
COMPUTER: DATENTING SYSTEM: DC CONSTITUTION NUMBER: US 07/618,314
FILING DATE: 05-UN-1995
CLASSIFICATION NUMBER: US 07/618,314
FILING DATE: 05-UN-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 05-UN-1996
ATTORNEY/AGENT NUMBER: 05-UN-1996
ATTORNEY/AGENT NUMBER: 05-UN-1996
ATTORNEY/AGENT NUMBER: 05-UN-1997
REJECHMONT CATION NUMBER: 05-UN-1997
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 05-UN-1996
ATTORNEY/AGENT NUMBER: 05-UN-1996
TELECOMMUNICATION INFORMATION:
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Patent No. 5801044
GENERAL INFORMATION:
APPLICANT: Seed et al., Brian
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TOPOLOGY:
US-08-461-968A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CACAGAAGTICCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313
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                                                                                                                                              1 AGGIGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGACCTGGGTCCTCGGTAAAGGTCT
                                                                                                       Gaps
                                                                                                     12;
                                                              Length 2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN'-LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSED: Fish & Richardson P.C.
STRRET: 225 Franklin Street
CITY: Boston
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30. CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
                                                              Score 293.2; DB 2;
Pred. No. 7.4e-83;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00786/284001
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02210-2804
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                            Query Match
Best Local Similarity 88.2%;
Matches 335; Conservative
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NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
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US-08-462-571-1
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                                                                                                                                                                                                                                                                                                                                                                                                                             133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGTATGCTATCAGCTGGGTGCGACAGGCCC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGACAAGGGCTTGAGTGGATGGGATGGGATCATCCCTATCTTTGGTACAGCAAACTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433
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APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: Mcafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTY: United States of America
COWNTYR: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                         Score 293.2; DB 5.
Pred. No. 7.4e-83;
0; Mismatches 33.
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FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 46, Application US/08652816A; Patent No. 5872215; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTGCTCATCGTCTCCTCA 368
                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
PCT-US96-10043-8
                                                                                                                                                                                                                                            79.7%;
                                                                                                                                                                                                                                            Query Match 79.7
Best Local Similarity 88.2
Matches 335, Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 2287 base pair
TYPE: nucleic acid
STRANDEDNESS: single
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Indels
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76.3%; Score 280.8; DB 2;
Best Local Similarity 85.7%; Pred. No. 38-79;
Matches 312; Conservative 0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312-474-6300 JFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
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US-08-652-816A-44
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Best Local Similarity 86.0%; Pred. No. 9.4e-80;
Matches 313, Conservative 0; Mismatches 51; Indels 0,
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Sequence 44, Application US/08652816A
Sequence 47, Application US/08652816A
Patent No.:5870-100
SETTION: Objourn, JK
APPLICANT: Objourn, JK
APPLICANT: Mcdafferty, JG
APPLICANT: Mcdafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
                                                                                     PFILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA: DCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA: US 08/244,597
FILING DATE: 01-UN-1994
ATTORNEY/GBRY INFORMATION:
NAME: DAVID W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
NAME: 369 ASS 010 NO: 46:
SEQUENCE CHARACTERISTICS:
LEBERONCE CHARACTERISTICS:
LEMETHER ASS 05 DATE: CAUBLE CONCLOST.
APPLICATION NUMBER: GB 9206318.9 FILING DATE: 24-MAR-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9206372.6 FILING DATE: 23-SEP-1992
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TOPOLOGY:
US-08-652-816A-46
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NUMBER OF SEQUENCES:

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                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic No. 5874299-Human Animals Capable of Producing Heterologous Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B: William M. Smith
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Codes for peptide of SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 280.8; DB 2;
Pred. No. 4e-79;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/07/834,539
                                                                                                                                                                                                                                                                                                                                                                    Sequence 53, Application US/08800353
Patent No. 5874299
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/834,
FILING DATE: 1992-02-05
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 96.0%;
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Product
TITLE OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Sm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: San Francisco
STATE: California
COUNTRY: USA
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 241..335
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 372..677
COTHER INFORMATION:
US-08-800-353-53
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                                                                                                          301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                                                               242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGGGATGTTCTC 301
                                                                                                                                                    302 ATAATTATGAGCTTTACTACTACTACATGGACGTCTGGGGCCAGGGGACAATGGTCACCG 361
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologus Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Codes for peptide of SEQ ID NO
                    241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/834,539A
FILING DATE: 1992-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Sequence 53, Application US/07834539A
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
TATTORNEY/AGENT INFORMATION:
NAME: Smith, William
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-543-5043
INPORMATION FOR SEQ ID NO: 52
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
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Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , LOCATION: 372.677; CCATION: 072.677; CCHER INFORMATION: CCUS-07-834-539A-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CITY: San Francisco
STATE: California
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LOCATION: 241..335
OTHER INFORMATION:
FEATURE:
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385 AGGTCCAGCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGTCCTCGGTGAAGGTCT 444
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                                                                                                                                                                                                                  CTGGACAAGGCTTGAGTGGATGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564
                                                                                                                                                                                                                                                                                   CACAGAAGTTCCAGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCTACA.240
                                                                                                                                                                                                                                                                                                                                                                                        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
                                                                                                                CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC
                                                                                                                                                                                 CTGGACAAGGGCTTGAGTGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 231, Application US/09042353
| Patent No. 6255458
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Lonberg, Nils
| APPLICANT: Kay, Robert M. Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies NUMBER OF SEQUENCES: 421
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Two Embarcadero Center, Eighth Floor STREET: California
| COUNTRY: VUSA. California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIDENTY: 1.08A

COMPUTER READBLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/904,668
FILING DATE: 13-UN-1992
PRIOR APPLICATION NUMBER: US 07/900,860
FILING DATE: 16-DEC-1993
PRIOR APPLICATION NUMBER: US 08/053,131
FILING DATE: 23-JUN-1992
PRIOR APPLICATION NUMBER: US 08/053,131
FILING DATE: 22-JUN-1993
PRIOR APPLICATION NUMBER: US 08/056,762
FILING DATE: 2-JUN-1993
PRIOR APPLICATION NUMBER: US 08/155,301
FILING DATE: 2-JUN-1993
PRIOR APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
FILING DATE: 10-DEC-1993
FILING DATE: 10-DEC-1993
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US-09-042-353-231
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181.CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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OTHER INFORMATION: /product= "human V-HI family OTHER INFORMATION: gene V-H49.8"
US-09-042-353.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.3%; Score 280.8; DB 4; 96.0%; Pred. No. 4e-79; live 0; Mismatches 12;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MRR.1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1996
FILING DATE: 10-OCT-1996
FILING DATE: 10-OCT-1996
FILING DATE: 10-OCT-1996
FILING DATE: 10-OCT-1996
FILING DATE: 07-DEC-1996
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US-08-758-417A-79
; Sequence 79, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 96.0
Matches 288; Conservative
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385 AGGTCCAGCTCGTGCAGTCTGCGGCTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444
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                                                                                                                                                                                                                                                                                                                                                                                      181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCGTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nobert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06185
FILING DATE: 1991088
CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
NAME: Smith, William M.
REGISTRATION
NAME: 87654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.3%; Score 280.8; DB 5; 96.0%; Pred. No. 4e-79; tive 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53, Application PC/TUS9206185 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 1464
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTER.STICS:
LENGTH: 812 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: William M. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 96.0
Matches 288; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 372..677

COTHER INFORMATION:

PCT-US92-06185-53
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OTHER INFORMATION:
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STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGTCCTCGGTGAAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC
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                                                                                                                                                                                                                                                                                                                                 COMPUTEY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-0CT-1996
APPLICATION NUMBER: US 08/54,404
FILING DATE: 10-0CT-1995
APPLICATION NUMBER: US 08/32,322
FILING DATE: 09-MR-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-DEC-1993
APPLICATION NUMBER: US 08/16,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/16,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/15,301
FILING DATE: 12-UL-1993
APPLICATION NUMBER: US 08/05,762
FILING DATE: 22-UL-1993
APPLICATION NUMBER: US 08/05,762
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/05,762
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/05,762
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 576-0200
15) 576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 812 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
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INFORMATION FOR SEQ ID NO: 79
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Best Local Similarity 96.0
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415)
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Best Local Similarity 96.0%; Pred. No. 4e-79;
Matches 288; Conservative 0; Mismatches 12; Indels
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LOCATION: 241..285
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445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504
                                        CTGGACAAGGGCTTGAGTGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                                                                         505 CTGGACAAGGGCTTGAGTGGATGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564
                                                                                                                                                    565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACCAACA 624
                                                                                                                                                                                                                                         625 IGGAGCIGAGCAGCCIGAGAICIGAGGACACGGCCGIGIATIACIGIGCGAGAGACACAG 684
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 200 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY: USA
ZIP: 94105
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPUTER: IBM FC COMPATIBLE
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENTIN NATE: US/08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 11-DEC-1992
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 023
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 023
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 415-356-2402
THELEPHONE: 415-356-2402
                                                                                                                                                                                                                                                                                                                         US-08-053-131-61
; Sequence 61, Application US/08053131
; Patent No. 5661016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERLSTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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373..678
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NAME/KEY:

LOCATION:

FEATURE:

NAME/KEY:

LOCATION:

LOCATION:

US-08-053-131-61
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                                                                                         386 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT
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1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGTCCTCGGTAAAGGTCT
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US-006-645-641-61
Sequence 61, Application US/08645641
Patent No. 5719032
Patent No. 5719032
Patent No. 5719032
Patent No. 5719032-Human Animals for TITLE OF INVENTION: Transpenic No. 5719032-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSER: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER: Ploppy disk
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COMPUTER: Ploppy disk
COMPUTER: San Francisco
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: BOOSTIS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSIFICATION NUMBER: US 07/904,068
FILING DATE: 20-MA-1996
FILING DATE: 23-JUM-1992
ATTORNEY/ADREY INPORMATION:
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 30,223
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REFERENCE/DOCKET NUMBER: 30,223
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REPRENCE/DOCKET NUMBER: 30,223
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LOCATION:
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61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
                                          Length 813;
                                                                              Indels
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                                      Score 280.8; DB
Pred. No. 4e-79;
0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
                                      Query Match
Best Local Similarity 96.0%;
Matches 288; Conservative
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    US-07-853-408B-61
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Patent No. 5798550
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
                                      Length 813;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318
FLING DATE: 19920318
CLASSIFICATION: 800
ATTONREY/AGENT INPORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/POCKET UNBER: 14643-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                      Score 280.8; DB 1;
Pred. No. 4e-79;
0; Mismatches 12;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
                                      76.3%;
                                  Query Match
Best Local Similarity 96.0°
Matches 288; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: NUCLEIC ACID
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NAME/KEY:
LOCATION:
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LOCATION:
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61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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                                                                                 JENGTH: 813 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: Single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 241..285
FEATURE:
NAME/KEY: CDS
LOCATION: 373..678
US-08-096-762-61
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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Search completed: July 18, 2003, 19:59:08 Job time: 20.5137 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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July 18, 2003, 04:46:48; Search time 1002.03 Seconds (without alignments) 10397.705 Million cell updates/sec 1 gigcagciggiggagictgg...........358 4109280 2054640 seqs, 14551402878 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 em_ro:*
em_ats:*
em_un:*
em_htg.hum:*
em_htg.inv:*
em_htg.inv:*
em_htg.old:*
em_htg.pin:*
em_htg.pin:*
em_htg.rod:*
em_htg.mam:*
em_htg.wrt:*
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em_htg.old:*
em_htg.old:* US-09-627-896B-30 358 Minimum DB seq length: 0 Maximum DB seq length: 200000000 1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ow:* fun: em om: GenEmbl:* Scoring table: Perfect score: Database : Sequence: Searched: Run on:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description		pie	X62965 H.sabie	AF174030 Homo	AF062138 Homo	AJ300/96 HOMO 214189 H.sanie	AB067237 Homo	X63850 H.sapie		U80083 Human	U76679 Homo sa	AJ300785 AF062188	AX001146 AX001146 Sequence	AJ300781 Homo 8	AF062241 Homo sap	U96282 Homo san	Z14175 H.sapi	AJ300779	AFUBZIIS HOMO	AJ300783 Homo	U00487 Human		Z37291 H.sapie		AFI/4118 HOMO A:7238038 HOMO	U80084 Human		AFUEZIZI HOMC U00584 Human	114 X65896 H.sapi	ď.,	X61646 Human To	AF174095 Homo s	AF174034 Homo s	AB063913 Homo	HSIGT219 X67908 H.sapiens r	ALIGNMENTS		tip		g reg	IgG;		Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.	
Length DB	•	357 9	351 9	20 9	50	7 60	9	72 9	. 6 . 27	48	60 09	54 72 9	14 6	51 9	0 0	0 0	6 49	54	727	54 9	78 9	51.0	78 9	73 9	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	6 09	000	51 70 90	11 9	09	000	6 99	05 9	63	17 9			DNA for ant:		7:	.ન ≿્ર		etazoa; theria;	
* Query Match		74.7	73.7	73.4	72.9	72.8	72.2	72.2	71.9	71.6	71.6	71.3	71.1	71.0	70.8	70.7	70.7	4.07	70.2	70.0	70.0	7.00	9.69	69.4	2.69	68.9	68.9	68.8	68.7	68.4	4. 4.	68.4	68.3	68.2	68.1			HSVH3H2FG H.sapiens	dion, sub	X70485 X70485.1 GI:3844 anti-DNA antibody	ain; Ig	no sapiens no sapiens	Eukaryota; Mammalia;	
Score	} ;		93.4	262.6	7	9 6		58.	57.	56.	. 55	55.	254.6	54.	23	25.	25		51.	50.	900	. O	24		4 7	46.	46.	4 4 5 6	45.		4 4		44	24	243.8		1 FG	_			che imi		Eu} Man	
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Query Match
Best Local Similarity
Matches 313; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GACTCTGTGAAGGGCCGATTCACCATCTCCAGGGACAACGCCAAGAACTCACTGTATCTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA--GATCTGT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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1 (bases 1 to 1679)

Strausberg, R.

Strausberg, R.

Submisted (0'-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive; Room 11A03, Bethesda, MD 20892-2590, NIH-MGC Project URL: http://mgc.nci.nih.gov
           Smith, A.
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Manheimer-Lory, A., Katz, J.B., Pillinger, M., Ghossein, C., and Diamond, B.
Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
J. Exp. Med. 174 (6), 1639-1652 (1991)
92078875
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Matches 315; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAL plate: 40 Row: i Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
BX Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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11arity 86.9%; Pred. No. 2.4e-74;
Conservative 0; Mismatches 45
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/translation="WELGLGWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAAS
GFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQM
NSLRAEDTAVYYCARDGDIGDWWFDPWGQGTLVTVSSG"
                                                                                                                                                                                                                                              AF174030 420 bp mRNA linear. PRI 08-MAY-2001 Homo sapiens clone 77u-c17 immunoglobulin heavy chain variable region precursor (IgH) mRNA, partial cds.
                                                                     GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243
                                         CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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/codon_start=1
/product="immunoglobulin heavy chain variable region
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Catarrhini; Hominidae; Homo
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Pred. No. 6e-74;
0; Mismatches 44; Indels 3;
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(clone lib="77u"
...>420
                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrat Mammalia; Butheria; Primates; Catarrhini; Hominid 1 (bases 1 to 420)
Mang,x and Stollar,B.D.
Immunoglobulin VH gene expression in human aging Clin. Immunol. 93 (2), 132-142 (1999)
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Wang,X. and Stollar,B.D.
Direct Submission
Submitted (02-AUG-1999) Biochemistry De
School of Medicine, 136 Harrison Ave.,
Location/Qualifiers
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/organism="Homo sapiens"
/db xref="taxon:9606"
/chromosome="14"
/map="14932.33"
/clone="77u-c17"
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/db_xref="GI:5834020"
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/gene="IgH"
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       358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (31-007-1991) F.M. Raaphorst, Division of Immunology, Dept. of Immunohematology and Bloodbank, Academic Hospital Leiden, Bulding 1, E3-Q, P.O.Box 9600, 2300 Leiden, THE NETHERLANDS For related sequences see X62954-X62972, X53612-3, M37277, Schroeder H.W. Ur. et al., Proc.Natl.Acad.Sci.USA, 87:6149(1990) & Ichihara y. et al, Eur. J. Immunol. 18:649(1988).
                                       423 AGCTGGTACAGGGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 482
                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (basea I to 351)
Raaphorst, F.M. Timmers, E., Kenter, M.J., Van Tol, M.J., Vossen, J.M. and Schuurman, R.K.
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299 TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACGTCTCCTCA
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Ig CDR3 region; Ig heavy chain; Jh element; rearranged gene;
                                                                                                                                    HSVH31328 351 bp mRNA linear PRI H.sapiens rearranged mRNA for fetal IG heavy chain Vh3, unidentified D (or N) region and Jh4 (clone FL13-28).
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/tissue_type="liver"
/dev_stage="13 week old foetus"
1. 296
/note="Vh element"
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/isolate="Clone FL13-28"
/db_xref="taxon:9606"
/chromosome="14"
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/note="Jh element"
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/note="CDR3"
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us-09-627-896b-30.rge

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Losses 1 to 351)
Leucht, S., Uttenreuther-Fischer, M. M., Gaedicke, G. and Fischer, P. The B cell superantigen-like interaction of intravenous immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30 germline gene origin cloned from a patient with Kawasaki disease is enhanced after IVIG therapy

(21185274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSA300796 351 bp mRNA linear PRI 10-APR-2001 Homo sapiens partial mRNA for immunoglobulin gamma heavy chain variable region (IGHV3-7), clone M2-129 (m2hie129), Kawasaki disease patient.
AJ300796 1 GI:12733998 AJ300796.1 GI:12733998 AJ300796.1 Wariable region.
                                                                                                                                                                     241 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAAGAGCAAGAAACTCACTGTATCTG 300
                                                                                                                                                                                                                                                                                                                                                                240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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Direct Submission
Direct Submitted (17-3An-2001) Fischer P., Charite Children's Hospital,
Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
Berlin, 10117, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                                                                                                                                                                                                                                              GGGAAGGGCTGGAGTGGCTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG
                                                                                                                                              TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
                                                                                                                                                                                                                     GGGAAGGGGCTGGAGTGGTTGATATATAATGGTAGTCGGAATTGAACCATACTATGCG
                                                                                                                                                                                                                                                                                          GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
                                                                         1 GTGCAGCTGGTGGAGTCTGGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                                                                                                        Grecaecregarerosesesasecrregrecaecreseseseseseserecreaaacrere
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                                     Gaps
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/fenci="immune response"
/codo.start=1
/product="immunoglobulin gamma heavy chain variable
                                     3;
  9; Length 420;
                                     45; Indels
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/organism="Homo sapiens"
/isolate="Kawasaki disease patient"
/db_xref="taxon:9606"
/clone="M2-129 (m2hie129)"
/cell_type="B cell"
/rearranged
Score 261; DB 9;
Pred. No. 2e-73;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="IGHV3-7"
  Query Match 72.9%;
Best Local Similarity 86.6%;
Matches 311; Conservative
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Fischer, P.
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/product="immunoglobulin heavy chain variable region"
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GFTFGSYMMSWWRQAPERGLEWWANIKQDGSERYYDDSWRGRFTISRDNAKNSLYLQM
NSLRAEDTAVYYCAVTIVVVPAAPDYWGQGTLVTVSSG"
                                                                                                                                                                                                                                                                                                                                                                                                                                 AF062138 420 bp mRNA linear PRI 08-MAY-2001 Homo sapiens clone 45u-11 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.
AF062138.1 GI:3170738
                                       TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                             GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
                                                                                                                                                                                CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
                                                                                                                                                                                                                                                         1 (25.70)
Wang,X. and Stollar,B.D.
Wang,X. and Stollar,B.D.
Direct Submission
Submitted (22-ARR-1998) Biochemistry Department, Tufts University
School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dassa 1 to 420) and Stollar, B.D. Immunoglobulin VH gene expression in human aging Clin. Immunol 93 (2), 132-142 (1999)
                                                                                                                                                                                                                                                                                                         CITATGACAGAGGCTACTITGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                                                                                                                                                                                                                                                                                                                              ATATCGGTGACTGCGTGCGTTCCGACCCCTGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="14"

/map="44912.33"

/clone="45u-11"

/cell_type="peripheral B lymphocyte"

/issue_type="blood"

/note="from elderly repertoire 45u"
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/gene="IGH"
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/gene="IGH"
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<1. >409
/codon start=2
/product="Ig heavy chain variable region (VDJ)"
/procuct="Ig heavy chain variable region (VDJ)"
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RAEDTAVYYCARGLTGATDAFDIWGQGTMVTVSS"
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 259.4; DB 9; Length 409;
Pred. No. 6.5e-73;
0; Mismatches 46; Indels 3
                              /tissue type="feral liver"
/clone lib="ESS"
<1. .>409
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                                                                                                                                                                                                                                                                                 50. 343
/note="Ig V-segment"
344. 352
/note="Ig D-segment"
363. 409
/note="Ig J-segment"
a 90 c 134 9
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/note="signal peptide"
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ilarity 86.4%;
Conservative 0
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2 (bases 1 to 363)
Kurosawa, Y.
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                                                    /protein_id="CAC28901.1"
/db_xref=101:12733999"
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LEWVANIRQCSSERYYVDSVKGRFFTISRDNAKNSLYLGMNSLRAEDTAVYYCARDDSG
IFDYWGQGTLVTVSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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1 (bases 1 to 409)
Tonnelle,C.
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                                                                                                                                                           <1. .>351
/gene="IGHV3-7"
/product="immunoglobulin gamma heavy chain variable
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Cuisinier,A.M., Gauthier,L., Boubli,L., Fougereau,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H. Sapiens rearranged Ig heavy chain variable region (VDJ). Z14189. X65741 Z14189.1 GI:31005 Ig D-segment; Ig heavy chain; Ig J-segment; Ig V-segment; Homo sapiens Homo sapiens
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                                                                                                                                                                                                                                                                                                              Length 351;
                                                                                                                                                                                                                                                                                                            Query Match 72.8%; Score 260.6; DB 9; Length Best Local Similarity 87.2%; Pred. No. 2.6e-73; Matches 313; Conservative 0; Mismatches 34; Indels
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/db xref="taxon:9606"
/chromosome="14"
/clone="3.14"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 351)
Leucht, S., Uttenreuther-Fischer, M.M., Gaedicke, G. and Fischer, P. The Be call superantiqen-like interaction of intravenous immunoglobin (IUG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5
                                                                                                                                                                                                                    HSA300786

15.1 bp mRNA linear PRI 10-APR-200:
Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
variable region (IGHV3-7), clone MI-45 (mihie45), Kawasaki disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
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AJ300786.1 GI:12733975
IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki
variable region.
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Pred. No. 1.4e-72;
0; Mismatches 41; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                  /note="complementarity determining region, 145. 198 /note="complementarity determining region, 90 c 126 g 75 t
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                                bearing
and Diamond, B.
Molecular characteristics of antibodies anti-DNA-associated idiotype
J. Exp. Med. 174 (6), 1639-1652 (1991)
20708875
                                                                                                                                                                Location/Qualifiers
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ilarity 85.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAAGGGGCTGGAGTGGTGATATATATGGTAGTTGGAATTGAACCATACTATGCG 179
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Yammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 372)
Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 IGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                             1. .363
/organism="Homo sapiens"
/db_xref="teaxon:9606"
/clone="yaOl16h"
/clone lib="AOl16h"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Immunology; Kutsukake-cho, Toyoake, Aichi 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please višt our web site University our web site University (buy.fujita-hu.ac.jp/immunity/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 258.4; DB 9; Length 363;
Pred. No. 1.4e-72;
0; Mismatches · 46; Indels 2;
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| db_xref="d1:1273976"
| translation="MYQLLESGGGIVOPGESIRLSCAASGFTFSSYGMSWVRQAPGKG
| LEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSIRAEDTAVYYCAREVAG
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                                                                                                                         2 (bases 1 to 351)
Bischer, P.
Bischer, P.
Bischer, Submission
Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital,
Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
Berlin, 10117, GERMAN
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germline gene origin cloned from a patient with Kawasaki disease enhanced after IVIG therapy Clin. Immunol. 99 (1), 18-29 (2001) 21185274
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/gene="IGHV3-7"
/product="immunoglobulin gamma heavy chain variable
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/product="immunoglobulin gamma heavy chain variable
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                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/isolate="Kawasaki disease patient"
/db_xref="taxon:9606"
/clone="M1-45 (mlhie45)"
/celi type="B cell"
/rearranged
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Pred. No. 2.9e-72;
0; Mismatches 36;
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/gene="IGHV3-7"
/function="immune response"
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Best Local Similarity 86.6%;
Matches 311; Conservative
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Human immunoglobulin heavy chain variable region (V3-07) gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGTTGCTACTAT 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 gerresegaarrarraracecririsecracisesegasecas
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                           Human immunodeficiency virus type 1 Viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid 1 (bases 1 to 375) 1 (bases 1 to 375) 1 (bases 1 to 375) 1 Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120 patent: WO 0100678-A 33 04-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7, GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 GGGAAGGGGCTGGAGTGGCTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCT--
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Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo
                                                                                                                                                                                                                                                                                                                /organism="Human immunodeficiency virus type 1"
/db_xref="taxon:11676"
/note="VH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 256.6; DB 6; Length 375;
Pred. No. 5.2e-72;
0; Mismatches 44; Indels 11
                                                                                                                                                                                                                                 THE GOVERNMENT OF THE UNITED STATES OF AMERICA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glas, A.M., Nottenburg, C. and Milner, E.C.B.
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Human immunodeficiency virus type 1.
Human immunodeficiency virus type 1
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85.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                90
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 85.1
Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
PUBMED
REFERENCE
AUTHORS
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/ 5360
/codon start=1
/product="IGM heavy chain variable region"
/product="IGM heavy chain variable region"
/protein_id="AAB18977.1"
/db xref="GT:1673597.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGAAGGGGCTGGAGTGGTTAATATATGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 CAAATGAACAGCCTGAGAGCCGAGGACACGCGTGTATTACTGTGCGAGAGGATCTGT 299
241 CAAATGAACAGCCTGAAAGAACATGACAACAGCCATTATATACTGTG-GAGGGTTCGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease;
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                              . Virgen del Rocio, Immunology, 41013
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 354)
Leucht, S., Uttenreuther-Fischer, M.M., Gaedicke, G. and Fischer, P.
The B cell superantjagn-like interaction of intravenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 IGIGCAGCCTCTGGATTCACCTTTAGTAGCTTTTGGCTGAAACTGGGTCCGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GTGCAGCTGGTGGAGTCTCGGGGAGGCTTGGTCCCGCCTCGGGGGTCCCTGAGACTCTCC
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     autoreactive monoclonal
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IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki
variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 71.6%; Score 256.2; DB 9; Length 360; Best Local Similarity 85.8%; Pred. No. 7e-72; Matches 308; Conservative 0; Mismatches 48; Indels 3
                                                                                                               112/8825

2 (bases 1 to 360)

Aguilera, I.

Direct Submission
Submitted (30-OCT-1996) Hospital U. V
Manuel Siurot s/n, Seville, Spain, 41

10-Ocation/Qualifies

10-360
/ Crant = "Homo sapiens"
/ Ab xref="ttaxon:9606"
/ clone="COC-lhc"
/ cll type="hybridoma"
/ 1. >360
     structure of eight human
                 antibodies
Immunology 102 (3), 273-280 (2001)
21195372
11298825
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HSA300785
LOCUS
DEFINITION
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ORIGIN
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ORGANISM
                                                JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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VERSION
KEYWORDS
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AUTHORS
TITLE
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     TITLE
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                                                                                                                                                                                                                                   /cell type="CD19+ B cells"
/tissue type="peripheral blood"
/note="CD19+ peripheral blood B cells obtained from a bone marrow transplant recipient 90 days post transplant; clone in reference 1" .348
                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
Location/Qualifiers
1. 348
/ Organism="Homo sapiens"
/ Ab_xref="taxon:9606"
/ Ab_xref="taxon:9606"
/ Ab_xref="taxon:9606"
/ Ab_xref="taxon:9606"
/ Ab_xref="taxon:9606"
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Homo sapiens clone CDC-1hc IgM heavy chain variable region mRNA,
parcial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 GACTCTGTGAAGGGCCGATTCACCATCTCCCAGAGACAACGCCAAGAACTCACTGTATCTG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAAGGGGCTGGAGTGGTGGTTAATATAGTAGTTGGAATTGAAACCATACTATGGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACTCTGTGAGGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Fukaryota; Metazoa; Chimates; Catarrhini; Hominidae; Homo.

(bases 1 to 360)
Aguilera,I., Melero,J., Nunez-Roldan,A. and Sanchez,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 CITATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATATG-------GACTACTGGGGCCAGGAACCCTGGTCACCGTCTCTCA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 CAPATGAACAGCCTGAGGACCCGAGGCTGTGTATTACTGTGCGAGGGGCTCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.6%; Score 256.2; DB 9; Length 348; llarity 86.6%; Pred. No. 7e.73; Indels 15; Conservative 0; Mismatches 33; Indels 155
                                                                                                                                                                                                                                                                                                                                                                                                /gene="V3-07"
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Best Local Simi
Matches 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                   source
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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Homo sapiens
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                                                                           ORGANISM
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immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5 germline gene origin cloned from a patient with Kawasaki disease is enhanced after IVIG therapy Clin. Immunol. 99 (1), 18-29 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="dl:12733974"

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GHFDYWGQGTLVTVSS"
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                                                                                                              Fibruary Chamission
Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital,
Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
Berlin, 10117, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 TATGACAGAGGCTACTTTGACTACTGGGGCCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGTGGCT--
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product="immunoglobulin gamma heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="IGHV3-7"
/product="immunoglobulin gamma heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.3%; Score 255.4; DB 9; Length 354; 86.6%; Pred. No. 1.3e-71; ive 0; Mismatches 36; Indels 12;
                                                                                                                                                                                                                       /isolate="Kawasaki disease patient"

/db xref="taxon;9606"

/clone="M1-40 (mlhie40)"

/cell_type="B cell"

/rearranged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ų
                                                                                                                                                                                                                                                                                                                                                             function="immune response"
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                                                                                                                                                                                             1. .354
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                       protein_id="CAC28890.1"
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                                                                                                                                                                                                                                                                                                                  gene="IGHV3-7"
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Matches 309; Conservative
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PRI 08-MAY-2001

AF062188 372 bp mRNA linear PRI 08-MA: Homo sapiens clone 48u-19 immunoglobulin heavy chain variable

LOCUS DEFINITION

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RRVGTTYFDYWGQGTLVTVSSG"
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                                                                                                                                                Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
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80
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                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrai
Mammalia; Eutheria; Primates; Catarrhini; Hominic
1 (bases 1 to 372)
Wang, X. and Stollar, B.D.
Immunoglobulin VH gene expression in human aging
Clin. Immunol. 93 (2), 132-142 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="peripheral B lymphocyte"
/tissue_type="blood"
/note="from elderly repertoire 48u"
                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 372)
Wang,X. and Stollar,B.D.
Direct Submission
Submitted (22-ARR-1998) Biochemistry De
School of Medicine, 136 Harrison Ave.,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .372
/organism="Homo sapiens"
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/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAC18224.1"
/db_xref="GI:3170839"
  cds.
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region (IGH) mRNA, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="14q32.33"
/clone="48u-19"
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                       AF062188
AF062188.1 GI:3170838
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/gene="IGH"
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Best Local Similarity 85.0%;
Matches 311; Conservative
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353 TCCTCA 358 |||||| 364 TCCTCA 369

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Search completed: July 18, 2003, 13:47:39 Job time: 1004.03 secs

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AW401428 AW402648

BQ710073

BG758713

UI-HF-BKO AGENCOURT

BM713479 L AW402311 L BQ943156

AGENCOURT

602638142

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AGENCOURT

UI-HF-BK0

AGENCOURT UI-HF-BK0 AGENCOURT

AGENCOURT

BQ717993 BQ709776 AW403220 BQ708724 BM914366 AW403163

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Minimum DB Maximum DB

Database

Perfect score:

Seguence:

OM nucleic

Run on:

Scoring table:

AGENCOURT

BQ707419 AGENCOURT AW402029 UI-HF-BK0 BM914329 AGENCOURT

BG686716 BG538620 BQ709987

AGENCOURT

AGENCOUR UI-E-CII-

AGENCOURT

K-EST0049 AGENCOURT UI-HF-BK0

BQ711467 AW402613

BM767227

BG34059

602462161

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BG759119 704 bp mRNA linear EST 15-WAY-2001 602710759F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851063 5', mRNA sequence.
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FEATURES

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No. Result

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/tissue_type="placenta"
//note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
61 a 206 c 223 g 140 t 5 5 others
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BG756291.1 GI:14066944
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Eukaryota; Dutheria; Primates; Catarrhini; Hominidae; Homo.

In to Base 1 to 849 |

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCM7100 row: b column: 04

High quality Sequence stop: 778.
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/organism="Homo sapiens"

(db xrefe"taxon:9606"
    /clone="InMaGE:48510603"
    /clone="InMaGE:48510603"
    /clone="InMaGE:4810603"
    /clone="InMaGE:481060"
    /lissue type="Iprimary B-cells from tonsils (cell line)"
    /lab host="Drimary B-cells, Vector: pOTB7; Site_1: XhOI;
    Site_2: BCORI; cDNA made by oligo-dT priming)
    Site_2: BCORI; cDNA made by oligo-dT priming)
    Directionally cloned into ECORI/XhOI sites using the
    following 5' adaptor: GGCACGAG(G). Size-selected >500bp
    for average insert size 1.8kb. Library constructed by Ling
    Hong in the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscribt II RT (Life Technologies).
    Note: this is a NIH—MGC Library."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

SE 10,W B., Gruber.C.; Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqrefégenoscope.cns.fr., Web : www.genoscope.cns.fr.

Location/Qualifiers

Location/Qualifiers

Abordanism="Homo sapiens"

Abordanism="Homo sapiens"

Abordanism="Homo sapiens"

Albaref="taxon:9606"

Allone="CSDD1061YP03"

Allone="CSDD1061YP03"
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AL551886 GI GI:12890261
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BG756386 831 bp mRNA linear EST 15-MAY-2001 602715711F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855682 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 GGGAGGGGGTGGAGTGGCTGATAAAGGACGATGGAAGTGAAAATTCTATGCG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 TGTGAAGCCTCTGGATTCACGTTTAGTGGCCATTGGATGACCTGGGTCCGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GGGAAGGGGCTGGAGTGGGTGGTTAATATATGGTAGTCGGAATTGAACCATACTATGCG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1705 row: f column: 03
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 248.2; DB 14; Length 904; Pred. No. 7.6e-58; O; Mismatches 53; Indels 3;
                                           organism="Homo sapiens"
                                                                   xref="taxon:9606"
Location/Qualifiers
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Best Local Similarity 84.4%;
Matches 303; Conservative
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              /clone="IMAGE:483867"
/clone="IMAGE:483867"
/clone=lib="WIH MGC 48"
/tlssue_type="Primary B-cells from tonsils (cell line)"
/lab_host="Drimary B-cells; Vector: pdrB7; Site 1: Xho!;
/note="Organ: B-cells; Vector: pdrB7; Site 1: Xho!;
Site_2: BcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho! sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Strangene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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5', mRNA Fequence.
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NIH-WGC http://mgc.nci.nih.gov/.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2384 row: o column: 02
High quality sequence stop: 667.
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Pred. No. 4.4e-58;
0; Mismatches 45
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
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Best Local Similarity 85.0%;
Matches 305; Conservative
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1707 row: j column: 10 High quality sequence stop: 793.
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602716437F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856553 5',
mRNA sequence.
BG755960
BG755960.1 GI:140666613
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini; Hominidae, Homo.

1 (bases 1 to 853)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Email: Capabe-r@mail.nih.gov
Sensil: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Contact: Louis M. Staudt, M.D. Ph.D.
Contact: Arguert preparation: Ling Hong/Rubin Laboratory
con A. Library Preparation: Ling Hong/Rubin Laboratory
con A. Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Çlone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                 69.1%; Score 247.4; DB 12; Length Clarity 84.7%; Pred. No. 12e-57.
Conservative 7 ; Mismatches 46; Indels
       ity sequence stop: 790.
Location/Qualifiers
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BQ706683
AGENCOURT 7976366 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214494
5', mRNA Fequence.
BQ706683.1 GI:21845582
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.
1 (bases 1 to 888)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
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/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_l: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRIXIX and sites using the following 5, adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Supersoript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 950)

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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                      can
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 07 Plate: LLCM2381 row: column: 07 High quality sequence stop: 653.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 888;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
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Pred. No. 5.8e-57;
0; Mismatches 55;
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BQ711129
BQ711129.1 GI:21850028
EST.
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Tissue Procurement: Dr. Mark Watson
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/organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:6214494"
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259 c 248
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ilarity 83.8%;
Conservative
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/organism="Homo sapiens"
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/note="organ: spleen; Vector: poTB7; Site_1: XhoI; Site_2: KoCRI; cDNA made by voligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library.

NIH MGC Library.

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602712981F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852916 5',
mRNA sequence.
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cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MG clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3385 row: f column: 14
High quality sequence stop: 398.
High quality sequence stop: 398.
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Pred. No. 1.1e-56;
0; Mismatches 56;
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Mammalla, Butheria, Primates, Cat
1 (bases 1 to 770)
NIH-MGC http://mgc.nci.nih.gov/.
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Best Local Similarity 83.2%;
Matches 302; Conservative
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/db_xref="Laxon:96pens" / db_xref="Laxon:96pens" / db_xref="Laxon:96pens" / clone="InAGS:615340" / clone=lib="NIH MGC 113" / lab_host="Drgan: splen; Vector: pOTB7; Site_1: Xhol; Site_2: / lab_host="Organ: splen; Vector: pOTB7; Site_1: Xhol; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned inco EcoRI/Xhol sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerad M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausher, Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCN2384 row: D column: 13
High quality sequence stop: 654.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
11 hbases 1 to 895).
11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (
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BQ708566
LOCUS
DEFINITION
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                                       REFERENCE
AUTHORS
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JOURNAL
COMMENT
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/dlone="INAGE:4852916"
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Stransberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
MA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://inage.llnl.gov
Plate: LLCM1698 row: b column: 21
High quality sequence stop: 718.
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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Pred. No. 1.1e-56;
); Mismatches 42;
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AGENCOURT 7983184 NIH_MGC_113.
5', mRNA Sequence.
BQ710073
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EST.
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Best Local Similarity 84.4%;
Matches 303; Conservative
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BQ710073
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
          TITLE
JOURNAL
COMMENT
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BQ708566 934 bp mRNA linear EST 16-JUL-2002
AGENCOURT 7975980 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6214806
5', mRNA @equence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 GTGAAGGGGCTGGAGTGGGTGCCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GGGAAGGGGCTGGAGTGGGTGGTTAATATATAGGTAGTCGGAATTGAACCATACTATGCG
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                                                                                                                                                                                                     Gaps
                                                                                                                                                                                         8
Query March 68.0%; Score 243.6; DB 14; Length 895; Best Local Similarity 83.1%; Pred. No. 1.14-556; Matches 304; Conservative 0; Masmatches 54; Indels 8;
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Ω

δ g

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/organism="Homo sapiens"
/db xref="Laxon:9666"
/clone=line="IMAGE:627625"
/clone=line="IMAGE:627625"
/clone=line="MIH MGC 113"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: BCORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
                                                                    BQ708029
AGENCOURT_8352453 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277625
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 979)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2464 row: e column: 18
High quality sequence stop: 626.
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Best Local Similarity 88.2%;
Matches 276; Conservative
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                                                                                                                                         5', mRNA sequence.
BQ708029
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ORIGIN
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             RESULT 12
BQ708029
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TITLE
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/lab_host="DH10B" (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoR1; cDNa made by oligo-dr priming. Directionally cloned
into EcoR1/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley, using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                            Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence start: 6
High quality sequence storp: 653.
Location/Qualifiers
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11 HGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 1.4e-56;
0; Mismatches 54; Indels 8;
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      BQ708566.1 GI:21847465
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Best Local Similarity 83.1%;
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Gaps

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1 (Dases I to 443)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.inh.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the II M.A.G.B. Consortium/Link at:

www-bio.linl.gov/bbrp/image/image.html

Seq primer: MJ Forward.ac.
                                                                                                                                                                                                                        AW401428 443 bp mRNA linear EST 16-FEB-2000 UI-HF-BK0-aad-b-02-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone IMAGE:3053139 5', mRNA sequence.
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424 AACAACCAGCTGGTAGATTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
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67.5%; Score 241.8; DB 10; Length 443;
Best Local Similarity 83.3%; Pred. No. 2.9e-56;
Matches 299; Conservative 0; Mismatches 57; Indels 3;
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Graft Score 243.2; DB 12; Length 1164; Best Local Similarity 83.3*; Pred. No. 2.1e-56; Matches 300; Conservative 0; Mismatches 58; Indels 2;
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UI-HF-BK0-aav-b-10-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3055051 5', mRNA sequence.
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I (bases 1 to 50)
NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
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CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                                                                                 441
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CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by. M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbr/image/image.html
Seq primer: M13 Forward.
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                                            383 CCATGGTTCAGTTCTACTTTGACTACGGGCCAGGGAACCCTGGTCACCGTCTCA
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        430 ACTAGAGAGCTGGTATAAACTGGTCGGACCCTGGGCCAGGGAACCCTGGTCATCGTCTCC 489

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Search completed: July 18, 2003, 09:26:12 Job time : 622.38 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	Human HIV-1 monocl	Human clone A6 fus	Human interleukin	Anti-IL8 monoclona	Human anti-FAPalph	Anti-FAPalpha anti	Affinity matured c	Affinity matured c	DNA sequence of hu
	ID	2 AAF29077	0 AAV74274	2 AAH41661	2 AAH30007	4 AAK98398	4 AAK98407	4 ABK32988	4 ABK32986	4 ABK32983
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	Query Match 1	71.7	71.1	67.9	67.9	67.3	67.3	67.0	67.0	67.0
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Human immunoglobul Single chain Apo-2 Nucleotide sequenc DP54 VH gene. Hom Human anti-HER2/ne AAV293 anti-(MCP)-	DNA encoding anti- DNA encoding the h DNA encoding the h MAD 2741 heavy cha Human CDNA encodin TRO005 heavy chain	מ שמ	DNA encoding the h hCAT1 binding huma HCAT1 clone 25 ant TROO05 heavy chain TROO05 heavy chain Human anti-HERZ/ne Human anti-GPIIb/I	Human H.VI monocl ACZ885 antibody he IgG antibody 2.1.1 Human anti-CD40 mo MAD 6-2 heavy chai Nucleotide sequenc DNA sequence of he DNA encoding heavy
AAQ78945 AAV72533 ABL41734 AAQ89332 AAF75589 ABK14254	AAS03534 AAA46866 AAA46894 ABA94334 AAS22532 AAH30055	AAZ55614 AAQ36131 AAQ36331 AAA46864 AAA46890 AAA46896 AAA46896	AAA46891 AAZ38921 AAZ38770 AAH30056 AAH30057 AAF75587 AAF1153 AAF72335	AAF29079 ABL55674 ABX88453 ABA94330 AAF55226 AAF55240
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10 11 13 14 15	16 18 19 10 10 10 10			5 6 4 4 4 4 4 5 0 0 1 4 6 4 8

ALIGNMENTS

RESULT 1 AAF2907

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Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gp120; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                  Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 33.
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AAF29077 standard; DNA; 375 BP.
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Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

WPI; 2001-112438/12. P-PSDB; AAB62776.

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97DE-1028697
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                                                 The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gpl20. These can be used in diagnosis and therapy of HIV-1 infection.
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                                                                                                                                              Gaps
 HIV-1
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                                                                                                                       Query Match 71.7%; Score 256.6; DB 22; Length 375; Best Local Similarity 85.1%; Pred. No. 1.7e-61; Matches 314; Conservative 0; Mismatches 44; Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a human antibody (hAb) against a fusion (poly)peptide or protein that includes a segment of at least 6 consecutive His residues. This antibody is useful in Western blots, enzyme-linked immunosorbent assay (ELISA), immunofluorescence or immunoprecipitation assays. Also hAb can be used for affinity purification of the protein, for in vivo diagnosis or therapy, and in production of vaccines. hAb are universally applicable alternatives to human serum. They are specific for the polyhistidine tag, regardless of the nature of the rest of the protein. Since hAb are not produced in an animmal, they contain no components that can induce an immune response in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.1%; Score 254.6; DB 20; Length 814; Pred. No. 6.9e-61; Indels 5; Conservative 0; Mismatches 49; Indels 5;
                                                                                                                                                                                                                                                                                                               Human antibody against fusion protein with polyhistidine tag -
useful as standard in immunoassays, for affinity purification,
diagnosis and therapy and for preparing vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 814 BP; 181 A; 228 C; 232 G; 173 T; 0 other;
                                                                                  Kuerschner
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                                                                              Kipriyanov
(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
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                                                                              Ή,
                                                                              M, Doersam | Welschof M;
                                                                                                                                                                                                 WPI; 1999-106000/09.
P-PSDB; AAW90180.
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Best Local Similarity
Matches 309; Conserv
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Human antibody; detection; Fab; immunoglobulin; heterophilic antibody; human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes; target antigen; bacterial; fungal; viral; pathogen; human disease; hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria; Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; ds. ds. Detecting analyte in human sample containing human antibodies binding to nonhuman-antibodies, involves contacting sample with human antibody which binds to antibodies from nonhuman species and detecting binding Example 22; Page 88; 135pp; English. Gray J, DIAGNOSTICS INC 06-DEC-2000; 2000WO-US33042, 99US-0456090 Valkirs G, (BIOS-) BIOSITE DIAGN (GENP-) GENPHARM INT. WPI; 2001-374798/39 WO200140306-A1. sapiens. 06-DEC-1999; Buechler J, 07-JUN-2001 Synthetic. Homo

Lonberg N;

The present invention describes a method for detecting an analyte in a human sample containing human antibodies that specifically bind to antibodies from a nonhuman species. The method involves contacting the sample with a human antibody (1) which specifically binds to antibodies from a nonhuman species and detecting the binding between (1) and the analyte to indicate presence of the analyte. The method is used for detecting an analyte in a human sample containing human anti-mouse antibody (HAMA) (preferably human anti-mouse idotype antibodies and/or heterophilic antibodies). The method can also be used for detecting any type of target antibodies. The method can also be used for detecting any type of target antibodies or. The pertitis (A,B and C), influenza, Herpes, Glardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas that cause human antibodies can be used as detection reagents for performing clinical diagnostic tests and for performing other in vitro detection assays, including for research purposes. (1) can be used in qualitative assays designed to indicate the presence of one or more target antigen in a sample that usually correspond to indicate the presence of one or more assays for each target antigen. Also, (1) is used to determine the sample that usually correspond to the sensitivity limitations of the sense. Quantification of one or more target antigens in a sample can also be carried out using (1). AAH41612 to AAH41686, and AAB99361 to the present in the exemplification of the present incidence. invention

1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC Gaps 12; Score 243; DB 22; Length 675; Pred. No. 1.1e-57; Indels Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 other; 45; 0; Mismatches 67.9%; 84.1%; Matches 302; Conservative Query Match Best Local Similarity

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239 184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299 244 CAAATGAACAGCCTGAGGAGCCGAGGACACGCTGTGTAATTACTGTGCGAGAG------ 295 351 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG ---ATGGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCA 300 CITAIGACAGAGGCIACITIGACIACIGGGGCCAGGGAACCCIGGICACCGICTCCTCA 180 240 g g. 엄 ò ò

BP AAH30007 standard; DNA; 675 AAH30007; AAH30007 ID AAH3

(first entry) 19-JUL-2001

nucleotide fragment M1-23H. antibody Anti-IL8 monoclonal

human antibody phage display library; immunisation; transgenic animal; immunoglobulin; interleukin 8; IL8; immunogen; Human; antibody;

WO200125492-A1. Homo sapiens. Synthetic.

02-OCT-2000; 2000WO-US27237. 12-APR-2001

99US-0157415. 02-OCT-1999; 01-DEC-1999; BIOSITE DIAGNOSTICS INC. GENPHARM INT SUBSIDIARY OF MEDAREX INC (BIOS-) (GEND-)

Gray J, Lonberg N; Valkirs G, Buechler J,

WPI; 2001-335567/35.

Producing a human antibody phage display library comprises providing a transgenic animal whose genome comprises human immunoglobulin genes and isolating nucleic acids encoding antibody chains from lymphatic cells -

Example 22; Page 92; 161pp; English.

antibody phage display library (I), comprising: (1) providing a nonhuman transgenic animal (II) whose genome comprises human immunoglobulin genes; (2) isolating nucleic acids encoding human antibody chains (III) from lymphatic cells; and (3) forming a library of display packages whose members comprise a nucleic acid encoding (III) which is displayed from the package. The method is used for producing a human antibody display library, e.g., a Fab phage display library. The display method may be used to screen nucleic acids encoding antibody chains obstained from immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human monoclonal antibodies sequences used in the exemplification of the present invention. display library using this method means there is no need to immunise humans with antigens, and the difficulties faced with immortalising B cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056 The present invention describes a method (M1) for producing a human represent

Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 other;

Score 243; DB 22; Length 675; Pred. No. 1.1e-57; 67.9%; 84.1%; Best Local Similarity Query Match

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9 63 183 239 243 292 303

us-09-627-896b-30.rng

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same, such as inflammation and wound healing. The a coding sequence described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GAICIGICITAIGACAGAGGCTACTITGACTACTGGGGGCCAGGGAACCCTG 343
                                                                                                                                                                                                                                                                                                                         TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                                                                                                                                                                                                                                   64 TGTGCAGCCTCTGGATTCACCTTTAGTAACTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                GGGAAGGGGCTGGAGTGGTGGTTAATATAGTAGTAGTCGGAATTGAACCATACTATGCG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, FAPalpha, fibroblast activating protein alpha, antibody; Ab, gene therapy, cancer; wound healing, inflammation; cytostatic; gene,
                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mersmann
                                                                                                                                                                                   17;
                                                                                                                                   67.3%; Score 241; DB 24; Length 402;
llarity 82.1%; Pred. No. 3.5e-57;
Conservative 0; Mismatches 50; Indels 1
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                                                                                            81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-FAPalpha antibody fragment VH50YOLVLIII25 DNA.
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                                                                                            C; 124 G;
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11-SEP-2000; 2000GB-0022216.
                                                                                            Sequence 402 BP; 92 A; 105
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present sequence is the invention.
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P-PSDB; AAO14058.
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Best Local Similarity
Matches 308; Conserv
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Schmidt A;
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                                                                                                                                         119
                                                                                                                                                                   64 TGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123
                                                                                                                                                                                                                                GGGAAGGGGCTGGAGTGGGTGGTTAATATGGTAGTCGGAATTGAACCATACTATGCG 179
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                                                                                                                                                                                                                                                                                                                         180 GACTCTGTGAAGGGCCGATTCACCATGTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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                                                                                                                                                                                                                                                                                                                                                                                                              CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG----- 295
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gene therapy, cancer; wound healing, inflammation; cytostatic; gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human humanized antibody that specifically binds to fibroblasts activating protein alpha, useful for treating cancer or tumor, and for imaging tumors associated with activated stromal fibroblasts, e.g.·lung or breast cancer
                                               GTGCAGCTGGTGGAGTCTGGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                                                                               4 GTGCAGCTGGTGCAGTCTGGGGGGGGGGGGTCCTGGGGAGGTCCCTGAGACTCTCC
                                                                                                                                      TGTGCAGCCTC-GGATTCACCTTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ATGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACGTCTCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moosmayer D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human anti-FAPalpha antibody fragment VH50 DNA.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garin-Chesa P, Pfizenmaier K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 43; 109pp; English,
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11-SEP-2000; 2000GB-0022216.
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  302; Conservative
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P-PSDB; AAO14049.
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Schmidt
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                                                                          The present invention relates to a human or humanised antibody (Ab) which specifically binds to fibroblast activating protein alpha (FAPalpha). The antibodies are useful for preparing a composition for the treatment of cancer, and for imaging tumours associated with activated stromal fibroblasts, such as colorectal cancer, non-small-cell lung cancer, breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder cancer, pancreatic cancer and metastatic brain cancer, and diseases associated with the same, such as inflammation and wound healing. The present sequence is a coding sequence described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAAGACGCCAAGAACTCACTGTATCTG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAATGAACAGCCTGAGGGCCGAGGACACGGCTGTGTTACTGTGCGAGGGTTCACTC 303
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                imaging tumors associated with activated stromal fibroblasts, e.g. lung or breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                     GGGAAGGGGCTGGAGTGGCCAACATAAAGCAAGATGGAAGTGAAAATACTATGTG
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                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human antibody, immunoglobulin, Ig, variable heavy-chain; VH, variable light-chain; VL; anti-IL8; interleukin-8; scFV clone;
                                                                                                                                                                                                                                          DB 24; Length 788;
                                                                                                                                                                                                                                        Score 241; DB 24; Length 7
Pred. No. 4e-57;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                             CTGGGGGAGGCTTGGTCAAGCCTGGAGGGT
                                                                                                                                                                                                                  Sequence 788 BP; 191 A; 212 C; 212 G; 173 T; 0 other;
                                                      Page 46-47; 109pp; English
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                                                                                                                                                                                                                                          67.3%;
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nes 308; Conservative
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                                                                                                                                                                                            the invention
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                                                      Claim 90;
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Matches
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throughput generation and screening of a human antibody or immunoglobulin (Ig) library in yeast. The method comprises expressing a library of tester fusion proteins in yeast cells, each tester fusion protein comprises expressing a library of tester fusion protein activation domain or a DNA binding domain of a transcription activator and a tester protein having a large diversity within the library. The tester protein comprises a first polypeptide subunit (e.g. human variable heavy-chain, VH) whose sequence varies within the library, a second polypeptide subunit (e.g. human variable light-chain, VL) whose sequence varies within the library independently of the first polypeptide, and a linker peptide which links the first and second polypeptide subunits. The method is useful for generating with target antigens. The present DNA sequence represents an anti-ILB serv clone as described in the methods of the present invention.
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                                                                                                                                                                                                                                                                                                                    tester proteins against protein, peptide or using a two-hybrid method in yeast, useful for human antibodies and screening for their
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Pred. No. 7.5e-57;
0; Mismatches 45; Indels 26
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                                                                                                                                                                                                                                                                                                                       Screening libraries of tester proteins
                                                                                                                                                                                                                                                                                                                                                                                                        affinity binding with target antigens
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81.5%;
23-JUN-2000; 2000US-0602373.
23-JUN-2000; 2000US-0602972.
23-JUN-2000; 2000US-0603658.
23-JUN-2000; 2000US-0603663.
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es 313; Conserv
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GGAACCCTGGTCACCGTCTCCTCA 358
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23-JUN-2000; 2000US-0602972.
23-JUN-2000; 2000US-0603658.
23-JUN-2000; 2000US-0603658.
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                                                                                                                                                                                                                                                                                          23-APR-2002 (first entry)
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P-PSDB; AAU75149.
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                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to compositions and methods for high throughout generation and screening of a human antibody or immunoglobulin (Ig) library in yeast. The method comprises expressing a library of tester fusion proteins in yeast cells, each tester fusion protein comprising either an activation domain or a DNA blading domain of a transcription activator and a tester protein having a large diversity within the library. The tester protein comprises a first polypeptide subunit (e.g. human variable heavy-chain, WH) whose sequence varies within the library, a second polypeptide subunit (e.g. human variable heavy-chain, WH) whose sequence varies within the library independently of the first polypeptide, and a linker peptide which links the first of the first polypeptide subunits. The method is useful for generating econd polypeptide subunits. The method is useful for generating with target antigens. The present DNA sequence represents an anti-ILB scrv clone as described in the methods of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 TGTGCAGCCTCTGGGTTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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                                                                                                                                                                                                                                                                                                                                                                                                           Screening libraries of tester proteins against protein, peptide or nucleic acid target(s) using a two-hybrid method in yeast, useful f generating recombinant human antibodies and screening for their affinity binding with target antigens
                                                                                     Human antibody; immunoglobulin; Ig; variable heavy-chain; VH; variable light-chain; VL; anti-IL8; interleukin-8; scFV clone; ds.
                                                             Affinity matured clone M36-8 DNA from anti-IL8 scFv clone 123-36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Fig 20; 251pp; English.
                                                                                                                                                                                                                        25-JUN-2001; 2001WO-US20542.
                                                                                                                                                                                                                                                23-JUN-2000; 2000US-0602373.
23-JUN-2000; 2000US-0602972.
23-JUN-2000; 2000US-0603658.
23-JUN-2000; 2000US-0603653.
                                   23-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                 (GENE-) GENETASTIX CORP.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-090521/12.
P-PSDB; AAU75152.
                                                                                                                                                                                                                                                                                                                                            Zhu L, Hua SB;
                                                                                                                                                                    WO200200729-A2.
                                                                                                                               Homo sapiens.
Synthetic.
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The present invention relates to compositions and methods for high throughput generation and screening of a human antibody or immunoglobulin [1g) library in yeast. The method comprises expressing a library of rester fusion proceins in yeast cells, each tester fusion protein comprising either an activation domain or a DNA binding domain of a transcription activator and a tester protein having a large diversity within the library. The tester protein comprises a first polypeptide subunit (e.g. human variable heavy-chain, VH) whose sequence varies within the library, a second polypeptide subunit (e.g. human variable light-chain, VL) whose sequence varies within the library independently of the first polypeptide subunits. The method is useful for generating second polypeptide subunits. The method is useful for generating recombinant human antibodies and screening for their affinity binding with target antigens. The present DNA sequence represents an anti-lib scPV clone as described in the methods of the present invention.
                                                                                                                                                                                                                              -----CTTATGACAGAGGCTACTTTGACTACTGGGGCCAG 334
                                                                                                                                                                                                                                                                                               304 AGCAGTAGCTGGTCTTACTATGATAGTAGTGGTTATTACTACCCTGACTACTGGGGGCCAG 363
CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT
                                                                 244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGGAGAGTAAAGAGT
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variable light-chain; VL; anti-ILB; interleukin-B; scFV clone; ds.
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WPI; 1995-006791/01.
P-PSDB; AAR66301.
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                                                                                                                                                                                                                                 304 AGCAGTAGCTGGTCTTACTATGATAGTAGTGGTTATTACTACCCTGACTACTGGGGCCAG 363
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                                                                                                                                                                                                -----CTTATGACAGAGGCTACTTTGACTACTGGGGCCAG
                                                  GTGCAGCTGGTGGAGTCTGGGGGGGGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                                                                  TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
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                                                                                                                    GGGAAGGGGCTGGAGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG
                                                                                                                                    124 GGGAAGGGGCTGGAGTGGCTGGCCTACATAAAGCAAGATGGAAGTGAGAAATACTATGTG
                                                                                                                                                     GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
                                                                                                                                                                                      CAAATGAACAGCCTGAGGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGGATCTGT
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 '*tag= a
'product= Human immunoglobulin Variable heavy chain
                                                                                                                                                                                                                                                                                                                                                                                    Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain; cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "miscellaneous signal, does not conform to
terminator or splice site sequence"
                                  26;
               Score 240; DB 24; Length 795;
Pred. No. 7.5e-57;
0; Mismatches 45; Indels 20
Sequence 795 BP; 166 A; 211 C; 247 G; 171 T; 0 other;
                                                                                                                                                                                                                                                         GGAACCCTGGTCACCGTCTCCTCA 358
                                                                                                                                                                                                                                                                   Location/Qualifiers
184..638
                                                                                                                                                                                                                                                                                                                                                                   Human immunoglobulin Vh gene #7.
                                                                                                                                                                                                                                                                                                                    BP.
                Query Match
Best Local Similarity 81.5%;
Matches 313; Conservative
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638..640
/*tag= c
/note= "m:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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        - for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 67.0%; Score 240; DB 16; Length 877; Best Local Similarity 91.1%; Pred. No. 7.6e-57; Matches 266; Conservative 0; Mismatches 25; Indels
DNA fragment comprising human immunoglobulin Vh genes production of human immunoglobulin in mammalian hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 877 BP; 198 A; 207 C; 258 G; 214 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single chain Apo-2 antibody 20E6 encoding cDNA.
                                                                                                                            Claim 16; Page 39-40; 130pp; Japanese.
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1..939
/*tag= a
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/*tag= a /product= "single-chain Apo-2 antibody 20E6"

98US-0079029. 97US-046615P. 98US-074119P.

Location/Qualifiers

us-09-627-896b-30.rng

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The present sequence encodes a single-chain Apo-2 antibody, designated 20E6, which is isolated from a phage library. It is believed that Apo-2 is a member of the tumour necrosis factor receptor (TMRR) family. Apo-2 polypeptide is capable of triggering caspase-dependent appotosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cancer, to enhance immune-mediated cell death in cells expressing Apo-2, or setul and affainty purification of Apo-2 in specific cells, tissues or serum, and in affainty purification of Apo-2 from recombinant cell culture or natural sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding an Apo-2 ligand, useful for activating or stimulating apoptosis in cancer cells, thus especially useful in the treatment of cancer, or in enhancing immune-mediated cell death -
                                                                                                                     Human, Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
caspase; apoptosis; cancer; antibody; ss.
                                                                 Nucleotide sequence of single-chain Apo-2 antibody 20E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 14; Fig 15B; 68pp; English.
   29-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
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P-PSDB; ABB09604.
                                                                                                                                                                                                               Bacteriophage.
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09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes human Apo-2. Apo-2 can be used therapeutically to induce apoptosis in mammalian cells, and so is useful to the treat conditions associated with decreased apoptosis e.g. cancer.

Apo-2 is believed to be a new tumour necrosis factor (TNP) receptor.

The present conditions associated with decreased apoptosis e.g. cancer.

The proposition of the same apoptosis, thought to be initiated by binding to TNPRs, and Apo-2 triggered caspase-dependent apoptosis. It can be used to identify agents activating Apo-2, useful to treat therapeutically (e.g. those containing immunoglobulin sequences can be therapeutically (e.g. those containing immunoglobulin sequences can be inhibit apoptosis) or diagnostically (e.g. those comprising anti-tag cantibodies). It can be used to produce antibodies which can be combined with a (particularly pharmaceutically e.g. those comprising anti-tag cantibodies). It can be used to produce antibodies which can be combined or used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies). Agonistic (especially contained and antibodies can be administered to induce apoptosis in mammalian cancer cells, and anteagonistic antibodies used to block antibodies may also be used diagnostically e.g. to detect Apo-2 excession in cells/tissues and in Apo-2 purification. The present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor of the present comparisor 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GGGAAGGGGCTGGAGTGGGTGGTTAATAATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGACGAAGGCAAGAACTCACTGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTGCAGCTGGTGGAGTCTGGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                         Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions linked with decreased apoptosis e.g. cancer, and produce antibodies to increase or decrease apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Match 67.0%; Score 240; DB 20; Length 939; Local Similarity 91.1%; Pred. No. 7.7e-57; es 266; Conservative 0; Mismatches 25; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 939 BP; 218 A; 232 C; 287 G; 202 T; 0 other;
                                                                                                                                                                                                               Kim KJ;
                                                                                                                                                                                                               Chuntharapai A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 14; Fig 15B; 134pp; English.
98WO-US09704.
                                                          98US-0020746
97US-0857216
                                                                                                                                                                                                        Adams CW, Ashkenazi AJ,
                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                   WPI; 1999-045228/04.
P-PSDB; AAW83323.
   14-MAY-1998;
                                                          09-FEB-1998;
15-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
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                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GGGAAGGGGCTGGAGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 360
                                                                                                                                                                                                    GTGCAGCTGGTGGAGTCTGGGGGGGGGGGGCTTGGTCCTGGGGGGGTCCCTGAGACTCTCC
                                                                                                                                                                                                                                                                                                                    181 TGTGCAGCCTCTGGATTCACCTTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA
                                                                                                                                                                                                                                                                          TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
                                                                                                                                                             1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                                                                                                                                                                                                                                                                                                                                                                                        GGGAAGGGGCTGGAGTGGTTAATATATGGTAGTTGGAATTGAACCATACTATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
                                                Match 67.0%; Score 240; DB 24; Length 939; Local Similarity 91.1%; Pred. No. 7.76-57; Local Similarity 91.1%; On No. 7.76-57; Indels 18 266; Conservative 0; Mismatches 25; Indels 1
Sequence 939 BP; 218 A; 232 C; 287 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                          61
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                                                      Query Match
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ABL41,734 standard; DNA; 939 BP.

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ABL41734;

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The present invention provides the protein and coding sequences for human monoclonal antibodies which bind specifically to the HER2/neu growth factor receptor (also known as erbB2). These are designated 3-F2, 1-D2 and 2-B8. They can be used in the immunotherapy-based treatment and prognosis of cancers, particularly adenocarcinomas such as salivary gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas, and ovarian cancer. The present sequence is a coding sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GGGAAGGGGCTGGAGTGGTTAATATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAATGAACAGCCTGAGAGCCGAGGACACGCCGTGTATTACTGTGCGAGAGGGATCTG- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAATGAACAGCCTGAGAGCCGAGACACGGCTGTGTATTACTGTGCGCTTATGGTTCGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human monoclonal antibody that specifically binds to growth factor receptor HER2/neu, for treating, preventing or diagnosing diseases characterized by aberrant HER2/neu expression e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCAGCTGGTGGAGTCTGGGGAGACGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGTCATGCACTGGGTCCGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAAGAACACGCTGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTGCAGCTGGAGTCTGGGGGGGGTTCAAGCCTGGAGGGTCCCTGAAGCTCTCC
                                                                                                                                                                                                                                                                 Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy;
3-F2; 1-D2; 2-E8; growth factor receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 238.6; DB 22; Length 366;
Pred. No. 1.6e-56;
0; Mismatches 59; Indels 5;
                                                                                                                                                                                                             Human anti-HER2/neu antibody 2-E8 heavy chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 366 BP; 80 A; 87 C; 114 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 108; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                      AAF75589 standard; DNA; 366 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1999; 99US-0146313.
10-MAR-2000; 2000US-0188539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUL-2000; 2000WO-US20272
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 82.49
Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-168698/17.
P-PSDB; AAB72883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MEDA-) MEDAREX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deo Y;
                                                                                                                                                                                                                                                                                                                                                                                                  WO200109187-A2.
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                         10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-2001
                                                                                                          AAF75589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keler T,
     RESULT 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rerecascereresarreacerrrasrascrarrasarsascressreceseseseres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 2/15 clones of H chain (IgG1) genes showed homology to the germline gene DP54 (AAQ89313). The DNA (AAQ89333) and corresp. amino acid (AAR72075) sequences of the VH region of a representative clone, OF7H1.19, are provided.
361 CAAATGAACAGCCTGAGAGCCGAGGACACGCCTGTGTATTACTGTGCGAGAG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecular cloning of immunoglobulin genes by PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 239; DB 16; Length 294; Pred. No. 1.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H-chain DNA was amplified by PCR from Graves' orbital
                                                                                                                                                                                                                                                                                                                                              Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; autoimmunity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 294 BP; 69 A; 66 C; 98 G; 61 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 72; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NICH-) NICHOLS INST DIAGNOSTICS.
                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 91.1%;
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US10756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0124469
                                                                                                                              AAQ89332 standard; DNA; 294
                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                       DP54 VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-SEP-1993;
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Query Match

180 184 240

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Gaps

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304 GGACTTATTATAACGGGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a molecule that binds MCP-1 (human monocyte chemoattractant protein-1). The molecule has at least one antigen chinding site comprising at least one immunoglobulin (Ig) heavy and/or light chain variable domain (Wh, VI). The antibody of the invention preventing binding of MCP-1 (and also eccasin) to specific receptors, so preventing migration of monocytes and T cells. These are human antibodies with very high affinity for MCP-1, but no significant reaction with other human CC-type chemokines or MCP-1 from other species. The MCP-1 binding molecules, specifically antibodies that cross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound that binds human monocyte chemoattractant protein-1, useful e.g. for treating inflammation, comprises immunoglobulin chains with specific hypervariable regions
                                                                                                                                                                                                                                                                                                                          Human, antibody; MCP, monocyte chemoattractant, antiasthmatic, antiallergic, antiinflammatory, idiopathic thrombocytopennia, immunosuppressive, cytostatic, vasotropic, antiatreriosclerotic; antitheumatic, antiatritic; osteopathic, antigen-binding site; immunoglobulin heavy chain; monocyte migration; T cell migration; CC-type chemokine, eotaxin; allergy; allergic rhinitis; cancer; hypersensitivity response; allergic contact dermatitis; gene; inflammatory disease; asthma, psoriasis; COPD, osteoporosis; inflammatory disease; multiple sclerosis, autoimmune disease; rheumatoid arthritis; diabetes; systemic lupus erythematosus; home disease; osteoporosis, periodontal disease; heamatological disorder; haemolytic anaemia, graft rejection; leucocyte infiltration; restenosis; arteriosclerosis; AAV293; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Di Padova FE,
                                                                                                                                                                                                                                                                                               AAV293 anti-(MCP)-1 antibody heavy chain cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "AAV293 heavy chain protein"
/trans1 except= (pos:142.144, aa:Val)
/partia1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
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                                                                                                                                                                                    ABK14254 standard; cDNA; 366 BP
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P-PSDB; AAU75737.
                                                       TCA 358
                                                                                         TCA 366
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TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTTGGTCACCGTCTCC 355
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react with ectaxin, are used to prevent or treat MCP-1 or ectaxin-
mediated disorders, particularly those that involve migration or
activation of monocytes and T cells, e.g. allergies (allergic or in the state of the context dermatitis), inflammatory by a diseases (asthma, psoriasis, COPD, inflammatory bowel disease,
multiple sclerosis) autoimmune diseases of bone and cartilage of stepoprosis, orteoarthritis, periodothal diseases hammatory diseases of exteriors or systemic lupus erythematosus), diseases of bone and cartilage of sorteoarthritis, periodothal diseases) hammatological disorders (hammolytic anaemia, idiopathic thrombocycopaemia) graft rejection, cancers that include leucocyte infiltration, (re)stenosis, arteriosclerosis, osteoporosis and many other diseases listed in the specification. The present sequence represents the human AAV293 anti-(MCP) antibody heavy chain cDNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                       Sequence 366 BP; 78 A; 87 C; 118 G; 83 T; 0 other;
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US-10-040-244-14

US-09-927-122-41

US-09-927-1218-89

US-09-453-234-59

US-09-955-299-230

US-09-955-299-230

US-09-945-239-230

US-09-945-239-230

US-09-946-289-230

US-09-844-12

US-09-844-12

US-09-848-138-90

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US-09-848-798-91

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Publication No. US2003009195A1

GENERAL INPORMATION:

APPLICANT: Buechler, Joe

APPLICANT: Valkirs, Gunars

APPLICANT: Lonberg, Nils

APPLICANT: Lonberg, Nils

APPLICANT: GenPharm International

TITLE OF INVENTION: Human Antibodies

FILE REFERRNCE: 020015-00011008

CURRENT APPLICATION NUMBER: US/09/453,234

CURRENT FILING DATE: 1999-10-02

NUMBER OF FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 112

SEQ ID NO 67

LENDER PARTING OF 12

SEQ ID NO 67

LENDER APPLICATION VOWER: US/09/157,415

PRIOR FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 112

SEQ ID NO 67

LENDER PARTING FALE: 1999-10-02
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Best Local Similarity. 84.1%;
Matches 302; Conservative
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NAME/KEY: CDS
| LOCATION: (1)..(675)
US-09-453-234-67
      TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 2
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-811-737-24
US-10-052-798-7
US-09-972-656-67
US-10-153-382-8
US-10-153-382-4
US-10-153-382-4
US-10-153-382-1
US-10-153-382-1
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US-10-073-444-644-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 nucleic search, using sw model
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seq length: 200000000
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Pred. No.

Score

Result

9 63

Gaps

12;

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61 IGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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                                                                                                                                                                                                                                                                                                     Score 241; DB 10; Length 788; Pred. No. 1.7e-72; 0; Mismatches 50; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARER WINDER: WIDMATH.
CURRENT APPLICATION NUMBER: US/10/052,798
Patent No. US20020099180A1

GENERAL INFORMATION:

APPLICANT: Bochringer Ingelheim Pharma KG
TITLE OF INVENTION: Human FAP-alpha-specific antibodies
TITLE REFERENCE: 1-1129
CURRENT APPLICATION NUMBER: US/09/811,737
CURRENT FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 24

LENGTH: 788
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US-10-052-798-7
Sequence 7, Application US/10052798
Setulication No. US20020150985A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
APPLICANT: Adams, Annia W.
Chuntharapai, Annia J.
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Best Local Similarity 82.1%;
Matches 308; Conservative (
                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
US-09-811-737-24
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                                           GGGAAGGGGCTGGAGTGGTTAATATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                124 GGCAAGGGGCTGGAGTGGCTGGCAGCTATGTTGTTGATGGAAGTAAAACATACAATGCA 183
                                                                                                                          GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
                                                                                                                                                             184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243
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      64 TGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123
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                                                                                                                                                                                                                                                                                                            296 ---ATGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09811737

Patent No. US2002099180A1

GENERAL INFORMATION:

APPLICANT: Bookinger Ingelheim Pharma KG

TITLE OF INVENTION: Human FAP-alpha-specific antibodies

TILE REFERENCE: 1-1129

CURRENT APPLICATION NUMBER: US/09/811,737

CURRENT FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 32

SEQ ID NO 7

LENGTH: 402
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US-09-811-737-24
; Sequence 24 & Application US/09811737
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; ORGANISM: Homo sapiens
US-09-811-737-7
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Sequence 67, Application US/09972656
Fublication No. US20030099647A1
GENERAL INFORMATION:
APPLICANT: Deshpande, Rajendra
APPLICANT: Tsai, Mei.Mei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OF INVENTION: Neutralizing Activity
FILE REPERBNCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
                                                                                                                             120 GGGAAGGGCTGGAGTGGTTAATATATATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                             124 GGGAAGGGCTGGAGTGGCTGGCCAACATAAAGCAAGATGGAAGTGAAAATACTATGTG 183
                                                                                                                                                                                                                                                                                                                                                                                   180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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           GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGGTCCCTGAGACTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
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Matches 295; Conserv
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; LOCATION: (1)
US-09-972-656-67
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LENGTH: 672
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Publication No. US20030099655A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.;
APPLICANT: Tang, Ying
TITLE OF INVENTION: Related Methods;
TITLE OF INVENTION: Related Methods;
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529;
CURRENT APPLICATION NUMBER: US/09/995,529;
CURRENT APPLICATION NUMBER: US/09/995,529;
NUMBER: OF SEQ ID NOS: 358;
SOFTWARE: FastSEQ for Windows Version 4.0
FILING DATE: 02-No. US20020150985A1-2001
CLASSIFICATION: cunknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 67.0%; Score 240; DB 15; 3
Best Local Similarity 91.1%; Pred. No. 4e-72;
Matches 266; Conservative 0; Mismatches 25;
                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
                                                                                                                                                FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MASChang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 939 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-995-529-7
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US-09-995-529-7
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Publication No. US20030091561A1

GENERAL INFORMATION:

APPLICANT: van de Winkel, Jan G.J.

APPLICANT: van de Winkel, Jan G.J.

APPLICANT: derritsen, Arnout F.

APPLICANT: Gerritsen, Arnout F.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO

TITLE OF INVENTION: BEPIDERMAL GROWTH FACTOR RECEPTOR (EGFR)

FILE REFRENCE: GMI-020 100/10/172,317

CURRENT APPLICATION NUMBER: US/10/172,317

CURRENT FILING DATE: 2002-06-13

PRIOR FILING DATE: 2001-06-13

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 1

LENGTH: 375
                                                                                                                           Length 348;
                                                                                                                                                                                               45; Indels
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                                                                                                                  Ouery Match
66.2%; Score 237; DB 15;
Best Local Similarity 83.3%; Pred No. 3.1e-71;
Matches 299; Conservative 0; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-10-172-317-1
            ; LOCATION: (1)..(348)
US-10-324-493-15
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US-10-224-493-15

US-10-224-493-15

Sequence 15, Application US/1032493

Publication No. US20030124121A1

GENERAL INFORMATION:

APPLICANT: Pluenneke, John

TITLE OF INVENTION:

APPLICANT PAPLICATION NUMBER: US/10/944,493

CURRENT APPLICATION NUMBER: US/09/847,816

PRIOR APPLICATION NUMBER: 09/65,343

PRIOR PILING DATE: 2001-05-01

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2001-05-19

PRIOR PLING DATE: 2001-05-19

PRIOR PLING DATE: 2001-05-19

PRIOR PLING DATE: 2001-05-16

PRIOR PLING DATE: 2001-05-16

SOFTWARE: PAPLICATION NUMBER: 09/665,343

PRIOR PLING DATE: 2001-05-16

SOFTWARE: PAPLICATION NUMBER: 09/785,934

PRIOR PLING DATE: 2001-02-15

SOFTWARE: PAPLICATION NUMBER: 09/785,934

PRIOR PLING DATE: 2001-02-15

SOFTWARE: PAPLICATION NUMBER: 09/785,934

PRIOR PLING DATE: 2001-02-15

SOFTWARE: PAPLICATION NUMBER: 09/785,934

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SOFTWARE: PAPLICATION NUMBER: 09/785,934
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Sequence 8, Application US/10153382; Publication No. US2030086930A1; GENERAL INCOMMATION:
APPLICANT: PRIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES; FILE REFERENCE: PC23019A; CURRENT APPLICATION NUMBER: US/10/153,382; CURRENT FILING DATE: 2002-05-22; PRIOR APPLICATION NUMBER: 60/293042; PRIOR PILING DATE: 2001-05-23; NUMBER: OF SEQ ID NOS: 39; SOFTWARE: PALENT NOS: 39; SOFTWARE: PALENT NOS: 39; SOFTWARE: PALENT NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-153-382-8
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ORGANISM: Homo sapiens
FEATURE:
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CURRENT APPLICATION NUMBER: US/10/153,382
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                    CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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Best Local Similarity 82.2%;
Matches 295; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                ----GGATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCCAGGGAACCCTGGTC 346
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TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
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TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
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82.2%; Pred. No. 1.1e-69;
ive 0; Mismatches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/10153382; Publication No. US20030086930A1; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-153-382-1
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Best Local Similarity
Matches 295; Conserv
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                                                           Indels
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TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23.019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR APPLICATION NUMBER: 60/293042
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
Query Match 65.1%; Score 233; DB 15; Best Local Similarity 82.2%; Pred. No. 1.1e-69; Matches 295; Conservative 0; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 233; DB 15;
Pred. No. 1.1e-69;
0; Mismatches 55;
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FILE REFERENCE: 3005-C
CURRENT APPLICATION NUMBER: US/10/324,493
CURRENT PILING DATE: 2002-12-9
PRIOR APPLICATION NUMBER: US/09/847,816
PRIOR FILING DATE: 2001-05-01
PRIOR FILING DATE: 2001-05-01
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/665,343
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PARCELLY OF SEQ ID NOS: 26
SEQ ID NO 7
LENGTH: 354
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                      FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(354)

US-10-324-493-7
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; Publication No. US2030124121A1
; Publication No. US2030124121A1
; General Information:
; APPLICANT: Pluenneke, John
; TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
    61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 120
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                                                                           GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
                                                                                                   61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
US-10-153-382-2
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US-10-324-493-7
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180 GACTCIGIGAAGGGCCGATICACCATCICCAGAGGCAACGCCAAGAACTCACIGIATCTG 239
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                                                                                                                                               4 GTGCAGCTGGTGGAGGCTGGGGGGGGGGCGTGGTCCTGGGGAGGTCCCTGAGACTCTCC
                                                           6
Query Match
64 6%; Score 231.4; DB 15; Length 354;
BEEL Local Similarity 81.9%; Pred. NO. 2.6e-69;
Matches 294; Conservative 0; Mismatches 59;
Matches 294; Conservative 0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10073644C

Publication No. US20030082643A1

GENERAL INFORMATION:

APPLICANT: HUAGON, Debra

APPLICANT: van de Winkel, Jan

APPLICANT: van Dijk, Marc

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO FC ALPHA

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO FC ALPHA

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO FC ALPHA

TITLE OF INVENTION: NECEPTOR (CD89)

FILE REFERENCE: MILL 211

CURRENT PILLING DATE: 2002-21

PRIOR PILLING DATE: 2001-02-11

PRIOR APPLICATION NUMBER: US 60/288,075

PRIOR PILLING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Mindows Version 4.0

SEQ ID NO 1

LENGTH: 357
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ORGANISM: Homo sapiens
US-10-073-644C-1
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Search completed: July 18, 2003, 15:38:41 Job time: 87.5438 secs

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App Appl

Appl Appl Appl Appli Appli Appli Appl

49,

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Minimum DB Maximum DB

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Seguence 48, 1
Seguence 184,
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Honjo, Taguku
APPLICANT: Matsuda, Fuminiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCES: 145
CORRESPONDENCE ADDRESS:
Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUMTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR.1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY AGENT INFORMATION:
NAME: Freemen JOHN WANDER: DCT/JP93/00603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                         PCT-US93-10555-23
PCT-US93-10555-25
US-08-134-346A-49
US-08-134-346A-9
US-08-273-819A-9
US-08-428-197-29
US-08-428-197-29
US-08-428-197-31
PCT-US93-10555-32
PCT-US93-10555-32
PCT-US93-10555-31
US-09-240-274-192
US-08-468-671-1
US-08-468-671-1
US-08-545-809A-21
US-08-545-809A-21
US-08-545-809A-21
US-08-545-809A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08545809A Patent No. 6096878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REPRENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human İymphoblast
CGM1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
 TYPE: nucleic acid
STRANDEDNESS: double
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 July 18, 2003, 09:26:19; Search time 18.9834 Seconds (without alignments) 5783.490 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                              1 gtgcagctggtggagtctgg......scctggtcaccgtctcctca 358
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Sequence
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  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
  /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
  /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-240-274-90
US-08-157-101A-9
US-08-157-101A-6
US-09-240-274-91
US-09-240-274-91
US-09-240-274-88
US-09-202-181-3
US-09-202-181-3
US-09-202-181-3
US-09-202-181-3
US-09-202-181-3
US-09-202-320A-1
US-09-240-274-92
US-09-240-274-87
US-09-240-274-87
US-08-428-197-21
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PCT-US93-10555-19
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-08-958-201-7
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US-08-428-197-23
                                                                                                                                                                                                                                                                      441362 segs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        - nucleic search, using sw model
                                                                                                                                                                                                                          IDENTITY_NUC Gapop 10.0
                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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358
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2225.8 8 2225.8 8 2225.8 8 2225.8 8 2225.8 8 223.4 6 223.4 6 223.7 6 223.7 6 223.7 6 223.7 6 223.7 6 223.7 6 223.7 6 223.7 7 8 210.8 8 2117.8 8 2117.8 2117.6 2117.

Score

Result

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NS-09-240-274-89
) Sequence 89, Application US/09240274
) Sequence 89, Application US/09240274
) Patent No. 6255455
) GENERAL INFORMATION:
) APPLICATION: Sequence 80.
) TITLE OF INVENTION: Rh(D)-BINDING PROFIEINS AND MAGNETICALLY ACTIVATED CELL
) TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
) TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
) CURRENT PLING DATE: 1999-01-29
) EARLIER PILING DATE: 1999-01-29
) EARLIER PILING DATE: 1998-04-10
) EARLIER PILING DATE: 1996-10-11
) NUMBER OF SEQ ID NOS: 224
) SOFTWARE PARENTING UNCY: 2.0
) SEQ ID NO 89
ILBNGTH: 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 TGTGTAGTGTCTGGATTCACCTTCAATAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GGGAAGGGGCTGGAGTGGGTTAATATATATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------TGTCTTATGACAGAGGCTACTTTGACTACTAGGGGGCCCAGGGAACCCTGGTC 346
                      TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 Gecaagegecresagresergecagriatreserresarscaagraaraaracrareca 183
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                                                                                                                       180 GACTCTGTGAAGGGCGGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACACTGTACCTG
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                                                                                                GGGAAGGGGCTGGAGTGGTTAATATATGGTAGTCGGAATTGAACCATACTATGCG
                                                                                                                                                                             GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; Indels 14; Gaps
                                                                                                                                                                                                                                                   Query Match 63.7%; Score 228; DB 4; Length 375; Best Local Similarity 80.1%; Pred. No. 4.6e-60; Matches 298; Conservative 0; Mismatches 60; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: anti-Rh(D) chain D15
US-09-240-274-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                      61
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                                                                                     347 GTGCAGCTGGAGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGGTCCCTGAGACTCTCC 406
                                                                                                                                    TGTGCAGCCTC-GGATTCACCTTTACTAGGAÁTCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                           407 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 466
                                                                                                                                                                                                                 GGGAAGGGGCTGGAGTGGGTTAATAATAGTGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                     GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
                                                                                                                                                                                                                                                                                                                  1 GTGCAGCTGGTGGAGTCTGGGGGAGCCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   587 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTTTACTGTGCGAGAG 638
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Best Local Similarity 91.1%; Pred. No. 1.4e-63;
Matches 266; Conservative 0; Mismatches 25; Indels
Best Local Similarity 91.1%; Pred. No. 1.4e-63;
Matches 266; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk compuTER TREADABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
FLING DATE:
FLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MATECHANG, DIANE L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELEPAX: 650/952-9881
TELEPAX: 650/952-9881
TELEPAX: 650/952-9881
TELEPAX: 850/105-1081
TELEPAX: 39 base pairs
TYPE: Nucleic Acid
STRANDEDESS: Single
TOPOLOGY: Linear
US-09-079-029-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09079029;
Patent NO. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
APPLICANT: Abthenazi, Avi J.
APPLICANT: Chuntharapai, Avi J.
APPLICANT: Kim, Kyung J.
ITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCES: 16
STREET: DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-09-079-029-7
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                                                                                                                                       61
                                                                                                                                                                                                                                                                                           180
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61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rerecaecercreearreacerreagrageaarrerarecaeregegreegeceecaegereea 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 GGGAAGGGGCTGGAGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 GCCAAGGGGTTGGAGTGGGTGGCAGTTATATTATGATGAAATCATAAATTCTACGCA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GACTCCGTGAAGGGCCGATTCACCATTTCCAGAGACAATTCCAAGAACACACTGTATCTG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.1%; Score 225.8; DB 1; 80.5%; Pred. No. 3.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                               CORRESPONDENCE ADDRESS:
ADDRESSE: PILLSBURY, MADISON & SUTRO STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9437/204199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08157101A
Patent No. 5808032
GENERAL INFORMATION:
APPLICANT: KURIHARA, TATSUYA
APPLICANT: MATSUKURA, SHIGEKAZU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KURIHARA, TATSUYA
MATSUKURA, SHIGEKAZU
TSURUOKA, NOBUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARIMA, KENJI
NISHIHARA, TATSURO
                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 9.
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-861-3711
TELEFAX: 202-862-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1350 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 80.5
Matches 289; Conservative
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                  NUMBER OF SEQUENCES
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
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                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RN(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT PELING DATE: 1999-01-29
CURRENT PELING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER PILING DATE: 1996-04-10
EARLIER PILING DATE: 1996-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SEQ ID NOS: 224
SEQ ID NO 90
LENGTH: 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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TITLE OF INVENTION: ANTI-HB6 ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.2%; Score 226.4; DB 4; ilarity 79.8%; Pred. No. 1.4e-59; Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: anti-Rh(D) chain D16
US-09-240-274-90
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Patent No. 2808032
GENERAL INFORMATION:
APPLICANT: KURIHARA, TATSUYA .
APPLICANT: MYSUKURA, SHIGEKAZU
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
                                                                                                                                                                                    Sequence 90, Application US/09240274
Patent No. 6255455
364 ACCGTCTCCTCA 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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US-08-157-101A-9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
              셤
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Squence 77, Application US/09240274

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Squence 77, Application US/09240274

Squence 77, Application US/09240274

GREERL NO. 6255455

GREERL INFORMATION:
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: UNMBER: US/09/240,274

CURRENT APPLICATION NUMBER: 60/081,380

EARLIER PILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-10-11

SOFTWARE: PLEATION WUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

SOFTWARE: PLEATION VEY: 2.0

SSOFTWARE: PLEATION VOY: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 ------TGTCTTATGACAGAGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
304 ATAAAGCTATGGTCCGGATACTTTATACTTACTGGGGCCAGGGAACCCTGGTC 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 63.0%; Score 225.4; DB 4
Best Local Similarity 79.0%; Pred. No. 2.88-59;
Matches 296; Conservative 0; Mismatches 63
Matches 296; Conservative 0;
                                                                  CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER PILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
NUMBER OF SEQ ID NOS: 224
SEQ ID NO 91
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: anti-Rh(D) chain D17
US-09-240-274-91
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain D01
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ORGANISM: Homo sapiens
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225 GACTCCGTGAAGGGCCCATTTCACATTTCCAGAGAATTCCAAGAAAAACAACATGTATCTG 284
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Patent No. 625455
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Best Local Similarity 80.5%; Pred. No. 3.2e-59;
Matches 289; Conservative 0; Mismatches 67; Indels 3;
                                               ANTI-HBS ANTIBODY GENES AND EXPRESSION PLASMIDS THEREFOR
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND DATES.

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: DOC.
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: PatentIN Release #1.0, Version #1.25
COMPUTER READBLE FORM:
MEDIUM TYPE: PatentIN Release #1.0, Version #1.25
COMPUTER: DAFR-199
COMPUTER: DAFR-1994
COMPUTER: DAFR-1994
STILING DAFR: 05-ARR-1994
CLASSIFICATION NUMBER: 35843
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REFERENCE/DOCKET NUMBER: 9437/204199
TELEFORMINICATION INFORMATION:
TELEFAX: 6714627 CUCH
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TELEFAX: 1076 DAS EQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 DASE PAIFS
TYPE: UNDOCOUR: SINGle
STATE: DNA (Genomic)
US-08-157-101A-6
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US-09-240-274-91
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291 ------GGGATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACC 340
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                                                                                                                           GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG
                                                                                                                                                                                       184 GAGTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACTCCCAAGAACACACTGTATCTG
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Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and TITLE OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION DATA:
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
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FILING DATE: 0.2-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Sears Tower, 233 Sout CITY: Chicago STATE: Illinois COUNTRY: United States of America COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
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23-MAY-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 952'
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 961(
FILING DATE: 23-MAY: 1996
PRIOR APPLICATION DATA:
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SOFFILM METHOD FOR PRODUCTION THEREOF
FILE REPERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT PILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-04-10
EARLIER PILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PARENTIN Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GGGAAGGGGCTGGAGTGGGTGGTTAATATATGGTAGTCGGAATTGAACCATACTATGCG 179
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                                                                                                                                                                 14;
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                                                                                         DB 4; Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1e-58;
0; Mismatches 59; Indels
                                                                                                                                                             Indels
                                                                                                                    Pred. No. 4.3e-59;
0; Mismatches 62
                                                                                         Score 224.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 88, Application US/09240274
Patent No. 6255455
                                                                                      62.8%;
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                                                                                  Query Match 62.8
Best Local Similarity 79.6
Matches 296; Conservative
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Best Local Similarity 79.1
Matches 299; Conservative
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ORGANISM: Homo sapiens
US-09-240-274-77
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US-09-240-274-88
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| TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                           64 TGTGCACCGTCTGGATTCGTCTTCAGGAGTTATGGCATGCACTGGGTCCGCCCAGACTCCA 123
                                                                                                                                                            120 GGGAAGGGGCTGGAGTGGGTGATATATATGGTAGTCGGAATTGAACCATACTATGCG 179
                                                                                                                                                                                                                                      124 GGCAAGGGGCTTGAGTGGGTGTCACTTATATGGCATGATGGAAGTAATAGATTCTATGCA 183
                                                                                                                                                                                                                                                                                                                         180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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304 ATTGCAGCACCTGCTCCTCTGACCTCTGGGGCCAGGGAACCCTGGTCACCTCCTC 362
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APPLICANT: Irie, Reiko F
171LE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
171LE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY
NUMBER OF SEQUENCES: 1
CORRESPONDENCES: 1
ADDRESSEE: Pome, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
CONTY: Los Angeles
STREET: 2029 Century Park East, Suite 3800
CONTY: Los Angeles
STREET: 2029 Century Park East, Suite 3800
CONTY: Los Angeles
STREET: 2029 Century Park East, Suite 3800
CONTY: Los Angeles
COMPUTER: Rabballe FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFFWARE: WORDER: PC-DOS/MS-DOS
SOFFWARE: WORDER: US 07/609803
FILING DATE: 25-FEB-1993
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/609803
FILING DATE: 05-NOV-1990
ATTORNEY ACENT INFORMATION:
RAPELICATION NUMBER: US 07/609803
FILING DATE: 05-MANDER: US 07/609803
FILING DATE: 05-MANDER: US 07/609803
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ELL TYPE: Epstein Barr Virus Transformed B cell
CELL LINE: L612
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NAME/KEY: CDS
NAME/KEY: 1.432
CCCATION: 1.432
OTHER INFORMATION: /function= "Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08026320A
Patent No. 5419904
GENERAL INFORMATION:
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US-09-202-181-3
| Sequence 3, Application US/09202181
| Sequence 3, Application US/09202181
| Patent No. 6254867
| GENERAL INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, INFORMATION, IN
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62.3%; Score 223; DB 4; Length 36
Best Local Similarity 79.9%; Pred. No. 1.5e-58;
Matches 287; Conservative 0; Mismatches 70; Indels
Matches 287; Conservative 0; Mismatches 70; Indels
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (1)..(363)
US-09-202-181-3
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ORGANISM: human
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US-08-652-816A-22
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Query Match
Best Local Simi
Matches 294;
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                /product= "Immunoglobulin Variable Region"
/standard name= "HuMab L612 Heavy Chain Variable
Region Sequence"
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APPLICANT: Jackson, Paul J

APPLICANT: Lehnert, Bruce E

TITLE OF INVENTION: Distruption of Anthrax Toxin Binding to Cell

TITLE OF INVENTION: Receptors

FILE REFERENCE: S-89,662

CURRENT PAPLICATION NUMBER: US/09/273,839A

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Paterit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell
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                                                                                                                                                                                                                                                                                                                                   Length 432;
                                                                                                                                                                                                                                   0; Mismatches 69; Indels
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OTHER INFORMATION: /product= "Immunoglobulin Varial OTHER INFORMATION: /standard_name= "HuMab L612 Heav OTHER INFORMATION: Region Sequence"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 148._162
OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: determining region 1 (CDR1)"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 271..300
OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: determining region 2 (CDR2)"
FEATURE:
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Pred. No. 3.4e-58;
0; Mismatches 58;
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                                                                                                                                                                                                                                                                                                                                  62.2%; Score 222.6; 79.9%; Pred. No. 2.1
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Best Local Similarity 80.5%;
Matches 289; Conservative C
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Matches 287; Conservative
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CRGANISM: HOMO
US-09-273-839A-11
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US-09-273-839A-11
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LENGTH: 892
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GENERAL INFORMATION:

APPLICAMT: Siegel, Donald L.

APPLICAMT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2

CURRENT APPLICATION NUMBER: 60/940,274

CURRENT PILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-01-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PARENTIN Ver. 2.0

SEQ ID NO 92

LENGTH: 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 221.6; DB Pred. No. 4e-58; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: anti-Rh(D) chain D18
US-09-240-274-92
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; Patent No. 6255455
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ilarity 79.0%; Pre
Conservative 0;
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297 -----TGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
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TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SOFILING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT PAPPLICATION NUMBER: US/09/240,274
CURRENT PAPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-04-10
EARLIER FILING DATE: 1999-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PALCHIN VET: 2.0
SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 GGGAAGGGGCTGGAGTGGGTGATTAATAATGGTAGTCGGAATTGAACCATACTATGCG 179
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                                                                                       304 ATAAAGCTATGGTCCCGATACCTTTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 363
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Best Local Similarity 78.6%; Pred. No. 9.39-58;
Matches Cap?; Conservative 0; Mismarches 61; Indels 20
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; CTHER INFORMATION: anti-Rh(D) chain D13
VG-09-240-274-87
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Job time : 19.9834 secs
                                                                                                                                                                                                                                                                                                           Sequence 87, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                            RESULT 15
US-09-240-274-87
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